

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: David William Holden
- (ii) TITLE OF INVENTION: Identification of Genes
- (iii) NUMBER OF SEQUENCES: 501
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patrea L. Pabst
 - (B) STREET: 2800 One Atlantic Center
1201 West Peachtree Street
 - (C) CITY: Atlanta
 - (D) STATE: Georgia
 - (E) COUNTRY: USA
 - (F) ZIP: 30309-3450
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 01-DEC-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/637,759
 - (B) FILING DATE: 03-MAY-1996
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/GB95/02875
 - (B) FILING DATE: 11-DEC-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Pabst, Patrea L.
 - (B) REGISTRATION NUMBER: 31,284
 - (C) REFERENCE/DOCKET NUMBER: RPMS 101 CON 2
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (404) 873-8794
 - (B) TELEFAX: (404) 873-8795

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CTAGGTACCT ACAACCTCAA GCTTNKNKNK NKNKNKNKNK NKNKNKNKNK NKNKNKNKNK

60

NKNKAAGCTT GGTTAGAATG GGTACCATG

89

- (2) INFORMATION FOR SEQ ID NO: 2:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TACCTACAAC CTCAAGCT

18

- (2) INFORMATION FOR SEQ ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CATGGTACCC ATTCTAAC

18

- (2) INFORMATION FOR SEQ ID NO: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Synthetic oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TACCCATTCT AACCAAGC

18

- (2) INFORMATION FOR SEQ ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTAGGTACCT ACAACCTC

18

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CCTAGGCGGC CAGATCTGAT

20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Synthetic oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCACTTGTGT ATAAGAGTCA G

21

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGTCTTAATG TACGGGCATG GTCTGCATCG ATAACTCCGG CACGCAAATC GCCATCGATA

60

CTCATTGTGTT TGGCTGGCAT CCCATCAAGC GAGAAACGTG CGCTAACTTC CGCCACCCTC

120

TCGATACCTT TTGTAATGAC AATAAATTGC ACGATAGTAA TGATGGTAAA TACGACCAAC 180
 CCAACGGTGA GATTTCTCTCC TACGACAAAC TTACCGAAAG CATCCACAAA TATTACCGGC 240
 ATTATGTTGT AACAGTACCC AGCCGTGATG TGCTGATTGG GGAGTTAACA ACCGATTTAT 300

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCGCGGACGC TAGTGTGGTG GGTGACAGCC AGACGTTACC GAACGGGATG GGGCAGATCT 60
 GTTGGCTTAC AAAAGACATG GCCCATAAGG CGCAAGGTTT TGGGACTGGA CGTTTTCGCG 120
 GGCAGACAAC GTATCTCTGT CTTATTAAAA TGTGTCCTGC TTCGGCATAT GTATCGAACC 180
 CTCGGAGCAA AGTCGTTTGG GCGCAGAATT AGTACGTTTG GGTCCGTTGC TGTTATTCCT 240
 TGGGCTCGGA AAAAGAGTGC CAGCGTGAAG GAGTGGGATT TGGCAGACTG GCCGCCTAAT 300

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CACTATAGGG AAAGCTTGCA TGCCTGCAGG TCGACTCTAG AGGATCTACT AGTCATATGG 60
 ATTGCACTTG TGTATAAGAG TCAGGATTAG AGGACATGCG CCGGGAACCA TACTATCTTT 120
 TTCCGGTGCT TCGACGCCAT TTGCGGAAAC CACAGACTTT TTGCGGCGAA TGAGGATAAT 180
 TGGCAATGCT AACAACGCTG AAAAGAAAGC GAGAGTGATA AAAGGAAAGC CAGGAATTAA 240
 AGCGAGGAGC ATTAAAACCA CAGCGGCTAA TATGAGCGAC TGAGGTTGTC TGGCAATTTG 300

0974602-11600

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGCAGGCCGA CTCTAGAGGA TCCCCGGGTA CCGGTAATTT CTTTAACCTC GCATCCCCGGT	60
GGATGAAAGG ATATTCTGGC TGCCTAAGTA ATGAATGAAC CGCCAGTAG ATAAATATT	120
GAAAGTGATA ACCTGATGTT TTAATAACGA TGCAGGATAT ACATATAACA TGCTGGCATC	180
AAACCAGGTA AGCAAATCAT ATTGTGCTGC CAGGTTATTC AAATATCGA CCGGTGGTCC	240
AGGCGGGAAT TTTTCCACTA AATGTAGGTG GGATCAATGG GCTAATTGGT ATAGGCGGAT	300

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 324 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTGTGATTC CGGATGAAAT AGCTTTTACG AAAGCTGTCA GACNTGCTGA AGAATACGCT	60
GCAAATGGTA AGCTTGTAAC TTTTGGGTAT TGTTCCAACG CATGCTGAAA CGGGTTATGG	120
ATATATTCGT CGCGGTGAGT TGATAGGAAA TGACGCTTAT GCAGTGGCTG AATTTGTGGA	180
GAAACCGGAT ATCGATACCG CCCGTGACTA TTTCAAATCA GGGGAAATAT TACTGGCCTA	240
GCGGCGATGT TTTTATTTTCG CGCAAAGCCC TTATTTAAAC GAATTAAACG TATCTATCAC	300
CCCCAAATTC ATACAGCTTG TGAA	324

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

TTACTAAACA GGGCCCCGGA CCATGTAAAC ACCACGCTTG CCAACACTAA AAAACGATGC	60
TTGCCGTAAA AAAATTGAAC GTTATTTACT TAATACGCCT ATTTTATTTA CATTATGCAC	120
GGACAGAGGG TGAGGATTAA ATGGATAATA TTGATAATAA GTATACTCCA CAGCTATGTA	180
AAATTTTGGG GGCTATATCG GATTTGGTTG TTTTAAATTT AGCCTTATGG CTTTCACTAG	240
GATGTGTCTA TTTTTTTTGT GGTCAAGCAC AGAGATTTAT TCCCCAACCA CC	292

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TTTCCTTGCC GTGACAGTCC GGGATGCGAG GTTAACGAAA TTACCGGCAC CAAAGCTGTG	60
GAGGTGAGCG GTGTCCCCAG CTGCCTGACT CGTATTAGTC AATTAGCTTC AGTGCTGGAT	120
AATGCGTTAA TCAAACGAAA AGACAGTGCG GTGAGTGTA GTATATACAC GCTTAAGTAT	180
GCCACTGCGA TGGATACCCA GTACCATTAT CGCGATCAGT CCGTCGTGGT TCCAGGGGTC	240
GCCTAGTGTA TTGCGTGAGA TGAGTAACAC CAGCGTCCCG ACGTCATCGA CGAACAATGG	300

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATGAGTAAC CTACCCAAC	GTAATCTTTA CCAATATGCA TCATAATCTT CTGCTGGTAA	60
ATGATTGGTA ATATCGGAAA	GGTAAGTGAC ATAAGCACGC CATTACGTAA AAGTGCGGCC	120
CCTAAACTGC CACTTTTTAA	TAAGGGAAGT AATAAAGAAA GGCTCAATGG TCGAATAAAA	180
GCCACAGCCA ATGCAATAAG	CCACTCATTT ACCTGTTGTG CCATTCAACC ATGCTCTCCA	240
ATTTCGTAACA TTATCTGCCG	GGTATAATTC AACAGGATAC CGCTAAGCCA TGGGTAG	297

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 184 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ATTCCAGCCC CCGGGCCATC	TAACCACTAT GAACAATCAT CTTCTGGGTG GACAATCATT	60
GGTACCATCG GCCAGGCTTG	TGCAATATGT ATGTCATCAC GTAAAAGCGC GGCCCCTTAA	120
TCTCCCCATT CTTCTTAAG	GGCAGTTATC ACGGCTGGCT CAATGGCCGG CTTAACAGCC	180
ACAG		184

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GAGGCGCGTC TTCGGTTGAG	GGTCGCCCTC CAGATCTTTA TGCTCCTGTT TTACGTCATC	60
TTTACTCATT TTAAGATCTT	TTCTAATCTT ATAATATTGA AAAGAATAGT CCAGTATGCC	120
AACGACGAAA TAAAGAAACA	TCACCCCAAC CCATAACCAT TTTTCAATG ATGAAAGCAC	180

AAGCACGCCA	CAGGCTACAC	CACAGCCCGG	AGGGGGCCCG	AAAGTGCTGG	GATCTTGATT	240
AATGAAAAAG	GCAAAGGGAA	GAGATAGGAT	GATGCATGCT	GGTTGGAGGC	AGATTATTCA	300
TCTTCG						306

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

AGTTGCCGTA	TTTATTAAAT	ATTCACCTCA	GGTCAATATG	GAGGTCTTCC	CGGCTAAAAA	60
TCATTGCTTT	ACTAGAGATA	TCACTCCCTG	GGTTGCAATA	CAGTACGATT	AGTTATCTTG	120
ATGCAGCCTG	CTGATTTTCA	AATGGCAGCT	GACGTACCCG	CGAGACAAAC	ATTCTGGATT	180
ATGGACGTTA	TCAACGCCAA	TATAGGGAAG	GTGGTGAAGT	GGTTGATGAA	ATACCCCTAT	240
CCCTTGCAATG	TTATCGCTGA	CAGGACTGTT	ATCAGGAGCG	GGCATCCTCG	ATCGGCT	297

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAAGAGACAG	ATCCAAC TCG	GGCCGATCGC	CATAACGCCA	GCAGTTTGAA	AGATGAAAGC	60
CCAGCTTATC	CAGCCATTCC	GGTACAGCGT	AACGAGCAGG	TTGCCAGAAA	TAACGATAAA	120
GTTGCAACAC	CTCGGGATCA	GGTCGGCTCA	AAAACGGGGT	CTCAGGCAAA	AATAGCCGAT	180
CAGGATGCCC	ACTCCTAATA	ACAGTCCTGT	CAACGATAAC	ATCAACGGAT	AAGGGTATTT	240
CATCAACCAC	TTCACCACCT	TCCCTTTATT	GGCGTTGGAT	AACGTCCATA	ATCCAGA	297

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AGGGCTTTAT TGATTCCATT TTTACACTGA TGAATGTTCC GTTGCGCTGC CCGGATTACA	60
GCCGGATCCT CTAGAGTCGA CCTGCAGAAC CGAGCCAGGA GCAAATTAAT TTTTTTGGGC	120
AATTGCTGAA AGATGAAGCA TCCACCAGTA ACGCCAGTGC TTTATTACCG CAGGTTATGT	180
TGACCAGACA AATAGATTAT ATGCAGTTAA CGGTAGGCGT CGATTATCTT GTCAGAATAT	240
CAGGCGCAGC ATCGCAAGCG CTTAATAAGC TGGGTAACAT GGCATGAAGG GGCAACCC	298

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

CACTATAGGG AAAGCTTGCA TGCCTGCAGG TCGACTCTAG AGGATCTACT AGTCATATGG	60
ATTCTTAGGC GGCCAGATCT GATCAAGAGA CAGATCCAAC TCGGGCCGAT CGCCATAACG	120
CCAGCAGTTT GAAAGATGAA AGCCCAGCTT ATCCAGCCAT TCCGGTACAG CGTAACGAGC	180
AGGTTGCCAG AAATAACGAT AAAGTTGCAA CACCTCGGGA TCAGGTCGGC TCAAAAACGG	240
GGTCTCAGGC AAAAATAGCC GATCAGGATG CCCACTCCTA ATAACAGTCC TGTC AACG	298

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Partial sequence of Salmonella typhimurium
 virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```
CCCCCCCCCT TCTCCTGGCT TACACAGCCC CAGACCGGCG CTGGAAGG CCATTCCCGC      60
CATACAGGAG GCCAGCAACA TATTTTCACG CGCCGCCAGA TCGTGGCCGT AACCCACGGC      120
TTTCGGCAGC GATTTGCCAA TCATCGCTAT CGCGCCAATC GCCAGGCTGT CGGTAAACGG      180
CGTGGCGTTG AGCGCGCTGT AGGCCTCAAT CGCATGCGTC AACGCATCGA TACCGGTCAT      240
CGCCGTCACG TTTGGCGGAA CGCCTTCGGT CACGGAAGCA TCAAGAATCG CCACGTCCGG      300
C                                                                    301
```

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Partial sequence of Salmonella typhimurium
 virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

```
CGCGAACGTG CGCCGCAACT GCTTGTGGAC GGTGAATTGC AGTTTGACGC CGCTTTCGTG      60
CCGGAGGTCG CCGCGCAAAA AGCGCCTGAC AGCCCGCTGC AAGGCCGCGC CAACGTGATG      120
ATTTTCCCGT CGCTGGAGGC GGGCAATATT GGCTACAAAA TCACTCAGCG TCTGGGAGGC      180
TATCGCGCTG TTGGGCCGCT AATTCAGGGG CTTGGCGCGC CGCTTCACGA CCTCTCCCGA      240
GGCTGTAGCG TGCAGGAAAT TATCGAACTG CGGTTGGTGA GAAAACCAA                289
```

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Partial sequence of Salmonella typhimurium
 virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CGCCCTAGCA TGCCTGGCGT TGTCCGGTTA TTGCTCGTCA AGCGAACAGA TGCAAAAGGT 60
GAGAGCGACT CTCGAATCAT GGGGGGTCAT GTATCGGGAT GGTGTAATCT GTGATGACTT 120
ATTGGTACGA GAAGTGCAGG ATGTTTTGGA TAAAAATGGG TTACCCGCAT GCTGAAGTAT 180
CCAGCGAAGG GCCGGGGAGC GTGTTAATTC ATGATGATAT ACAAATGGAT CAGCAATGGC 240
GCAAGGTTCA ACCATTACTT GCAGATATTC CCGGGTTATT GCACTGGCAG ATTAGTCACT 300
CTC 303

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 300 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

CCCTTCCCAG GCTCGACAGG TACACAGCCA GCCACTGGTG CAGGCAGTTA CTTGCTTTCA 60
TCATGGGAAG GAGCAATATC CTGATATATT AAAGAAAGAG CGGGATCCCC TTTCTTTACT 120
GCTGCTAACG TTTCTTGCAA AATGCGTTGA TGAGATTCAT CCAGCACACC ACTGATAACA 180
AAAGAGCGCC GCATTGGCGT AACATTGACA AGCCCCACTA AACCGCTCTC TATTATCGCA 240
GAAATAATAT CATCCCCCTG AGACTGATGA GAGTGACTAT TCTGCCAGCG CAAATAACCC 300

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 303 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

ATACCGAGTA TTAAGCGGCT GTGTAACATC GTCATCCAAC AACATACGCA GCGAGCCGCC 60
ACGCCGAAA AACCGCATCG TGTCATGTGC CTGTTGTAGG GTCGGGTCTT TTTTCATGAG 120

TACGTTTTCT GCGCTATCAT ACTGGAAATT TCCCCCACT TACTGATAAG CCCTGTCAGT 180
TGGGTAAGGA CAGAGTTAAG CTCCTGAGAC ATTTTTTGGA ATGGTTATCT TTCCCCGACT 240
CATAAAATCG GTATTCCCGC TGGGGGCAAT ATCCAAAGAC GCTTTGGTCG CCCGTAGGGC 300
ACC 303

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GCCGTATGCC TGCAGTTGCC CGGTTATTGC TCGTCAAGCG AACCGATGCC AAAGGTGAGA 60
GCGACTCTCG AATCATGGGG GGTCAATGTAT CGGGATGGTG TAATCTGTGA TGAATTATTG 120
GTACGAGAAG TGCAGGATGT TTTGGTAAAA ATGGGTTACC CCCATGCTGA AGTATCCAGC 180
GAAGGGGCGG GGAGCGTGTT AATTCACGAT GATATTCAAA TGGGTCAGCA ATGGGGCAAG 240
GTTCAACCCC CACTTGCAGA TATTCACCCC CCTATTGGAC TGGCAGATTA GTCACTCTCA 300

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GGGCGACCTG CCCGCGGCGC AACTTTCCCC GAAGCGTTTT CCATTTCCCTT GTTCTTAAAT 60
GACCTGGAAA GCTTACCTAA GCCTTGTCCTT GCCTATGTGA CAATACTGCT TGGAGAACAC 120
CCGGACGTCC ATGATTATGC TATACAGATC ACAGCGGATG GGGGATGGTG AATCGGTTAT 180
TATACCACAA GTCGCAGCTC TGAGCTTATT GCTATTGAGA TAGAAAAACA CCCCCTTCA 240

ACTTGGATT TGAATAATGT AATACGCAAT CACCATACAC TATATTCGGG TGGCGTATAA 300

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

TTTCGAGCTGG GGCACCGCTA ATATCTTTAA CCTCGCATCC CGGTGATGAA AGGATATTCT	60
GGCTGCGTAA GTAATGAATG AACCGCCCAG CAGATAAAAT ATTGACAGTG ATAACCCGAT	120
GTTTTTTTAA CGATGCAGGC TATACATATA ACATAGCTGG CCACCAACAC AGCTGAAAGTA	180
AATCATATTG TTGCTGCCAG GCTACTTCAC ACTATTGTCC GGCGGGCCAG CGGGGATTTT	240
CCCCCTAAAT CTCGCTGGTT CTCAAA	266

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

AGTCTACGAT TTCGCTATAT CTTCTCTTAA TCATGGCCGC CATTTGTGGA TGCGATTTTA	60
AAATATCCGG GCGATCTTTC ATTAAAAAAT AAAGATTCCC CATGACTTCA CAGATAAAGG	120
TATCGGTATT TTGAGTGATA CGTAACAATT CGTTCTCTTC GTGTGGGTCC ATGATGCGAA	180
GAATAATGGT GGCATCATTT TCATGAGGAT TATGAACCCG AAATCTTTCT CTTTGCGATG	240
CGCAGGCTAA CTCTTTCAAC TCAAAAAA TCTCTGTAAG CCGCTCTCGT GTGGGGGCGC	300

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GCGCCCCTTT AATTGGTTGA GCGGCTGGT ATTCTTGTA GGGTAATACT AGCGAGACCC	60
AGGTTCCACC CCCGGGGACA CTTTTTAGTG TCAGATTACC GCCCATCATT TTAGCCAGGC	120
TTGACGCAAT AGTCAGTCCA ATTCCTGTAC CTTGCGAATT TGTGTCTGCT TGATAAAAAAG	180
CAGAAAAGAT TTGAGACTGC TGCTGTTTTT CAATCCCCC ACCGCTATCG CTAACCAGAA	240
ATATTAATTG TTCCTACCA AGATTGAGCG CCAGACGTAT CCCTCCCCC TCGGGAAAT	299

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GGATAAGATC CCGGATAAGT ATGTCAGGCT CGTATGCACA ACAGGCATTA TAAACCTCTA	60
GACCATTTTT AACATGCTCT ACTATTTTAA AATGAGGCCA GGGTAATAAG GCATTCATAA	120
TGCCGTTAAT GATGATTTC TAATCGTCTA CTAATAAGAT CTTATATTCT TTCATTTGGC	180
TGCCCTCGCG AAAATTAAGA TAATATTAAG TAATGGTGTA GGTGTGGAG ATCATACGTA	240
TTTTCTGGCG TAAGTCGGTT AGTTCCTCCA GCGCGATGAT TTTCCCCATT TTTACGCGAT	300

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 278 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Partial sequence of Salmonella typhimurium
virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

TTCCATATTG CTCGTCCGGG GAGCGTGTTA ATTCTTGATG ATATACCAAT GGATCTGCAA 60
TGGCGCAAGG TTCAACCATT ACTTGAGAT ATTCCCGGGT TATTGTACTG GGAGATTAGT 120
CACTCTCATC AGTCTCAGGG GGGTGATGTT ATTTCTGGGA TAATAGAGCA ACGGCGTTAG 180
CAGGGGTCGG TCAGTAGTCA CGGCCAACTT CGGTGCACTT TTGCGTATCA CTGGGGTATC 240
ATAACTGAAT CTCATCCCCC CCACTTTGGT AATCACAC 278

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

AATTCTTTTA CCTCCATAAG CTGCGTGGA TAGCGATACA GAGTATTAAG CGGGTGTGTT 60
ACATCGTCAT CCAACAACAT ACGCAGCGAG CCGCCACGCC GGAAAAACCG CATCGTGTCA 120
TGTGCCTGTT GTAGGGTCGG GTCTTTTTTTT CATGAGTACG TGTTCTGCGC TATCATACTG 180
GAAATTTCCC CCCACTTACT GATAAGCCCT GTCAGTTGGG TAAGGACAGC GTTAAGCTCC 240
TGAGACATTT TTTGAGTTGT TATCTGCCCC CCGACTCATA AGATCGGGTA TTCCGCGGTG 300
G 301

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 297 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Partial sequence of *Salmonella typhimurium* virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATATCCCTAA TGCTTTTCCT TAAAATAAAT ACCACGGAAG GATACTGGCC ACCTAGCCAA 60

ATTTAGAAAG CAATGAACAT CCGGTTTATT CCTGAAAACG ATTACTCCGG CGCACGTTGT 120
TCTGGCGTTA CCTGAGCCAG CAAACGATAT AATGGGGTGG TGACCCGCAT ACCGGTCATT 180
GGCATCCCAT CCACACCGGA GGGAGTAAAA CTCATTAGGC CATAGGTAAT ATCATTAAAGA 240
CGCTCTAATA AATGAGGGTG GGGGGCCCAA ACTACCACTC CAGTATGTAT TGAGTCA 297

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Partial sequence of Salmonella typhimurium virulence gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CCCATGGGCG CAATTTGTTG CGCAGCGTTT ACCCGACCAT CGCGTTTATG AGCTGTAATT 60
CATGGGGGGT AAAAACGGGC GTGACGACCC CAACGGAAGA TAAGGCCGGG CTTAAACAGG 120
AGATTATTGC TAATGCGCAG CGCAAAGTGT TGCTGGCGGA CAGCAGTAAG TATGGCGCGC 180
ATTCGCTCTT TAATGTGGTG CCGCTTGAGC GCTTTAATGA CGTGATTACC GACGTCAATC 240
TGCCGCCGTC AGCGCAGGTT GAACTGAAAG GGCGCGCTTT TTGCGCTAAC G 291

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DNA sequence of VGC II from centre to left hand end

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CTGCAGAACC GAGCCAGGAG CAAATTAATT TTTTGAACA ATTGCTGAAA GATGAAGCAT 60
CCACCAGTAA CGCCAGTGCT TTATTACCGC AGGTTATGTT GACCAGACAA ATGGATTATA 120
TGCAGTTAAC GGTAGGCGTC GATTATCTTG CCAGAATATC ACGGCGCAGC ATGCCAAGCG 180
CTTAATAAGC TGGATAACAT GGCATGAAGG TTCATCGTAT AGTATTTCTT ACTGTCCTTA 240
CGTTCTTTCT TACGGCATGT GATGTGGATC TTTATCGCTC ATTGCCAGAA GATGAAGCGA 300

ATCAAATGCT GGCATTACTT ATGCAGCATC ATATTGATGC GAAAAAAAC AGGAAGAGGA	360
TGGTGTAAAC TTACGTGTCG AGCAGTCGGC AGTTTATTAA TGCGGTTGAG GCTACTTAGA	420
CTTAACGGTT ATCCGCATAG GGCAGTTTAC AACGGCGGAT AAGATGTTTC CGGCTAATCA	480
GTTAGTGGTA TCACCCAGG AAGAACAGGC AGAAGATTAA TTTTAA GAAACAAAGAA	540
TTGAAGGAAT GCTGAGTCAG ATGGAGGGGC GTGATTAATG GCAAAAGTGA CCATTGCGCT	600
ACCGACTTAT GATGAGGGAA GTAACGCTTC TCCGAGCTCA GTTGCCGTAT TTATAAAATA	660
TTCACCTCAG GTCAATATGG AGGCCTTTTCG GGTAAAAATT AAAGATTAA TAGAGATGTC	720
AATCCCTGGG TTGCAATACA GTAAGATTAG TATCTTGATG CAGCCTGCTG AATTCAGAAT	780
GGTAGCTGAC GTACCCGCGA GACAAACATT CTGGATTATG GACGTTATCA ACGCCAATAA	840
AGGGAAGGTG GTGAAGTGGT TGATGAAATA CCCTTATCCG TTGATGTTAT CGTTGACAGG	900
ACTGTTATTA GGAGTGGGCA TCCTGATCGG CTATTTTTCG CTGAGACGCC GTTTTGTAGC	960
CGACCTGATC CCGAGGTGTT GCAACTTTAT CGTTATTTCT GGCAACCTGC TCGTTACGCT	1020
GTACCGGAAT GGCTGGATAA GCTGGGCTTT CATCTTCAA CTGCTGGCGT TATGGCGATC	1080
GGCCCGAGTT GGATCGTCTT CTTGACAGAG CGTTAAATAG ACTAAGAGGA AGCTCTGTTA	1140
TTCCAGCCTG TTTAAATGAC AGGCAAAAAC GGCAGGTTTCG TCTTGCGCCG CGTATATCGG	1200
CATTTGCCTT TGGGCTGGGA TTATTCAAAC TCAGGTGTAG TGACTATTTT ATGCTACCAG	1260
AGTATCGGCA ATTGCTTCTA CAGTGGTTTA GCGAGGATGA GATCTGGCAG CTATATGGTT	1320
GGTTGGGGCA AAGAGATGGC AAATTACTTC CTCCGCAAGT GATGCAACAA ACTGCATTGC	1380
AGATCGGTAC CGCCATTCTT AATCGGGAAG CGCATGACGA TGCGGGTTTT ACATGCGCTA	1440
TTAGTATTAT TACCCCTCC GCAGCGTATA CTTTGGCCGA AGACTTCTCT TACCGAGATT	1500
ATCTTCATGG AGCATTTGCT ATGAGTTTTA CTTCACTTCC TCTGACGGAA ATTAACCATA	1560
AGCTACCCGC TCGAAATATT ATTGAGTCAC AGTGGATAAC ATTACAATTA ACTTTATTTG	1620
CGCAAGAGCA ACAAGCTAAG AGAGTTTCAC ATGCTATTGT GAGCTCCGCT TACCGTAAGG	1680
CTGAAAAAAT CATCCGAGAC GCCTATCGTT ATCAGCGTGA ACAGAAAGTT GAGCAGCAAC	1740
AAGAAGTAGC GTGCTTGCCT AAAAATACGC TGGAAAAAAT GGAAGTGGAA TGGCTGGAAC	1800
AGCATGTAAA ACATTTACAA GACGATGAAA ATCAATTTTCG TTCATTGGTC GATCACGCAG	1860
CGCATCATAT TAAAAATAGT ATAGAACAGG TTCTGTTGGC CTGGTTTCGAC CAACAGTCGG	1920
TAGACAGTGT TATGTGCCAT CGTCTGGCAC GCCAGGCCAC GGCTATGGCG GAAGAGGGAG	1980

CGCTTTATTT	GCGTATTCAT	CCTGAAAAAG	AGGCATTGAT	GCGAGAACT	TTTGGCAAGC	2040
GGTTTACGTT	GATTATCGAG	CCTGGTTTCT	CTCCCGATCA	GGCTGAACTT	TCCTCAACAC	2100
GATATGCCGT	TGAATTTTCA	CTTTCTCGTC	ATTTCAACGC	GTTACTGAAA	TGGTTACGTA	2160
ATGGTGAAGA	TAAAAGAGGT	AGCGATGAAT	ATTAAAATTA	ATGAGATAAA	AATGACGCCC	2220
CCTACAGCAT	TTACCCCTGG	CCAGGTTATA	GAGGAACAAG	AGGTTATTTT	GCCTTCAATG	2280
TTAGCTCTCC	AGGAGTTACA	GGAAACGACG	GGGGCAGCGC	TCTATGAGAC	GATGGAAGAA	2340
ATAGGAATGG	CGCTGAGTGG	TAAACTGCGC	GAAAATTATA	AATTCACTGA	TGCTGAGAAA	2400
CTGGAGCGCA	GACAGCAGGC	TTTGCTGCGT	TTGATAAAAC	AAATACAGGA	GGATAATGGG	2460
GCAACGTTGC	GTCCGCTTAC	CGAAGAGAAT	AGTGATCCTG	ATTTACAGAA	TGCGTATCAA	2520
ATTATCGCTC	TTGCAATGGC	GCTTACTGCC	GGCGGGTTGT	CAAAAAAGAA	AAAACGCGAT	2580
TTGCAATCGC	AACTGGATAC	GTTACAGCGG	AGGAGGGATG	GGAACCTGCC	GTTTTTAGTT	2640
TACTGGAACT	TGGCGAAGTG	GATACCGTAC	GCTGTCTCTT	CTGAAGCGTT	TTATGCAACA	2700
GGCGATAGAC	AACGATGAAA	TGCCCTTATC	GCAGTGGTTC	AGACGCGTGG	CAGACTGGCC	2760
GGATCGCTGT	GAACGGGTCC	GTATTTTGCT	AAGAGCAGTA	GCCTTTGAAC	TTAGCATATG	2820
CATCGAACCC	TCGGAGCAAA	GTCGTTTGGC	CGCAGCATTA	GTACGTTTGC	GTCGTTTGCT	2880
GTTATTCCCT	GGCCTTGAAA	AAGAGTGCCA	GCGTGAGGAG	TGGATTTGCC	AGTTGCCGCC	2940
TAATACATTA	CTGCCGCTAC	TACTCGATAT	TATTTGTGAG	CGCTGGCTTT	TCAGTGATTG	3000
GTTGCTTGAT	AGACTTACCG	CTATAGTTTC	TTCATCGAAG	ATGTTCAATC	GGTTACTCCA	3060
ACAACCTGAT	GCGCAGTTTA	TGCTGATACC	CGATAACTGT	TTTAACGACG	AAGATCAACG	3120
TGAACAAATT	CTCGAAACGC	TTCGTGAAGT	AAAGATAAAT	CAGGTTTTAT	TCTGATACCT	3180
GGCTTTCAAT	ATTTAGGTAA	ATTGGCTTTC	TGGCTCATCA	TGAGGCGTCA	GGATGGATTG	3240
GGATCTCATT	ACTGAACGTA	ATATTCAGCT	TTTTATTCAA	TTAGCAGGAT	TAGCTGAACG	3300
GCCTTTAGCA	ACCAATATGT	TCTGGCGGCA	AGGACAATAT	GAAACTATCA	TAACGGTCGT	3360
ATTCTCTTAT	GTCAGATACT	CAAGCAAACC	TTCTTAGACG	AAGAACTGCT	TTTTAAAGCG	3420
TTGGCTAACT	GGAAACCCGC	AGCGTTCAG	GGTATTCCTC	AACGATTATT	TTTGTTGCGC	3480
GATGGGCTTG	CAATGAGTTG	TTCTCCACCT	CTTTCAGCT	CCGCCGAGCT	CTGGTTACGA	3540
TTACATCATC	GACAAATAAA	ATTTCNTGGA	GTCGCAATGC	GTTTATGGTT	AGGTGAGGGA	3600
GTCAGGGCGC	AACAGTGGCT	CAGTGTATGC	GCGGGTCGGC	AGGATATGGT	TCTGGCGACG	3660
GTGTTATTAA	TCGCTATTGT	GATGATGCTG	TTACCTTGTC	CGACCTGGAT	GGTTGATATC	3720

CTGATTACTA TCAACCTTAT GTTTTTCAGTG ATCCTGCTCT TAATTGCTAT TTATCTTAGT	3780
GACCCTCTCG ATTTATCGGT ATTTCCGTCT TTATTACTTA TTACTACATT ATATCGTTTG	3840
TCACTCACAA TCAGCACATC ACGGCTGGTA CTGTTACAAC ATAATGCCCG TAATATTGTG	3900
GATGCTTTTCG GTAAGTTTGT CGTAGGAGGA AATCTCACCG TTGGGTGTTGGT CGTATTTACC	3960
ATCATTACTA TCGTGCAATT TATTGTCATT AAAAAAGGTA TCGAGAGGGT GGCAGGAAGTT	4020
AGCGCACGTT TCTCGCTTGA TGGGATGCCA GGCAAACAAA TGAGTATCGA TGGCGATTTG	4080
CGTGCCGGAG TTATCGATGC AGACCATGCC CGTACATTAA GACAGCATGT CCAGCAGGAA	4140
AGCCGCTTTC TCGGTGCGAT GGACGGTGCG ATGAAATTTG TTAAAGGCGA TACGATTGCC	4200
GGTATTATTG TTGTTCTGGT GAACATTATC GGCGGTATCA TTATCGCTAT CGTACAATAT	4260
GATATGTCGA TGAGTGAGGC TGTTCACT TATAGCGTAC TGTCAATCGG AGATGGTTTA	4320
TGTGGGCAAA TTCCATCGCT GCTGATTTCC CTTAGCGCGG GAATTATTGT CACCCGTGTC	4380
CCGGGTGAGA AACGCCAGAA CCTGGCGACA GAGTTGAGTT CTCAAATTGC CAGACAACCT	4440
CAGTCGCTCA TATTAACCGC TGTGGTTTTA ATGCTCCTCG CTTTAATTCC TGGCTTTCCT	4500
TTTATCACTC TCGCTTTCTT TTCAGCGTTG TTAGCATTGC CAATTATCCT CATTCGCCGC	4560
AAAAAGTCTG TGGTTTCCGC AAATGGCGTC GAAGCACCGG AAAAAGATAG TATGGTTCCC	4620
GGCGCATGTC CTCTAATCTT ACGTCTTAGC CCGACGTTAC ATTCTGCCGA CCTGATTCGT	4680
GATATTGACG CCATGAGATG GTTTTTATTT GAGGATACCG GCGTCCCTCT CCCTGAGGTG	4740
AATATTGAGG TTTTGCCTGA ACCCACCAGAA AAATTGACGG TACTGCTATA TCAGGAACCC	4800
GTATTTAGTT TATCTATTCC CGCTCAGGCG GATTATTTAT TGATAGGCGC GGACGCTAGT	4860
GTGGTGGGTG ACAGCCAGAC GTTACCGAAC GGGATGGGGC AGATCTGTTG GCTTACAAAA	4920
GACATGGCCC ATAAGGCGCA AGGTTTTGGA CTGGACGTTT TCGCGGGCAG CCAACGTATC	4980
TCTGCCTTAT TAAAATGTGT CCTGCTTCGG CATATGGGAG AGTTTATTGG TGTTCAGGAA	5040
ACGCGTTATC TAATGAATGC GATGGAAAAA AACTACTCTG AGCTGGTGAA AGAGCTTCAG	5100
CGCCAGTTAC CCATTAATAA AATCGCTGAA ACTTTGCAAC GGCTTGATATC AGAGCGGGTT	5160
TCTATTAGAG ATTTACGTCT TATTTTCGGC ACCTTAATTG ACTGGGCGCC ACGTGAAAAA	5220
GATGTCCTGA TGTGACAGA ATATGTCCGT ATCGCGCTTC GTCGTCATAT TCTGCGTCGT	5280
CTTAATCCGG AAGGAAAACC GCTGCCGATT TTGCGGATCG GCGAAGGTAT TGAAAACCTC	5340
GTGCGTGAAT CCATTCGCCA GACGGCAATG GGGACCTATA CTGCGCTGTC GTCTCGTCAT	5400

AAGACGCAGA TCCTGCAACT TATCGAGCAG GCGCTGAAGC AGTCAGCCAA ATTATTCATT	5460
GTCACCTTCTG TCGACACCCG ACGTTTCTTG CGAAAAATTA CAGAAGCCAC CTTGTTCGAC	5520
GTACCGATTT TGTCATGGCA GGAATTAGGA GAGGAGAGCC TTATACAAGT GGTAGAAAGT	5580
ATTGACCTTA GCGAAGAGGA GTTGGCGGAC AATGAAGAAT GAATTGATGC AACGTCTGAG	5640
GCTGAAATAT CCGCCCCCG ATGGTTATTG TCGATGGGGC CGAATTCAGG ATGTCAGCGC	5700
AACGTTGTTA AATGCGTGGT TGCCTGGGGT ATTTATGGGC GAGTTGTGCT GTATAAAGCC	5760
TGGAGAAGAA CTTGCTGAAG TCGTGGGGAT TAATGGCAGC AAAGCTTTC TATCTCCTTT	5820
TACGAGTACA ATCGGGCTTC ACTGCGGGCA GCAAGTGATG GCCTTAAGCG ACGCCATCAG	5880
GTTCCCGTGG GCGAAGCGTT ATTAGGGCGA GTTATTGATG GCTTTGGTCG TCCCCTTGAT	5940
GGCCGCGAAC TGCCCGACGT CTGCTGGAAA GACTATGATG CAATGCCTCC TCCCGCAATG	6000
GTTTCGACAGC CTATCACTCA ACCATTAATG ACGGGGATTC GCGCTATTGA TAGCGTTGCG	6060
ACCTGTGGCG AAGGGCAACG AGTGGGTATT TTTTCTGCTC CTGGCGTGGG GAAAAGCACG	6120
CTTCTGGCGA TGCTGTGTAA TGCGCCAGAC GCAGACAGCA ATGTTCTGGT GTTAATTGGT	6180
GAACGTGGAC GAGAAGTCCG CGAATTCATC GATTTTACAC TGTCTGAAGA GACCCGAAAA	6240
CGTTGTGTCA TTGTTGTGCG AACCTCTGAC AGACCCGCCT TAGAGCGCGT GAGGGCGCTG	6300
TTTGTGGCCA CCACGATAGC AGAATTTTTT CGCGATAATG GAAAGCGAGT CGTCTTGCTT	6360
GCCGACTCAC TGACGCGTTA TGCCAGGGCC GCACGGAAAT CGCTCTGGCG CCGGAGAGAC	6420
CGCGGTTTTCT GGAGAATATC GCCAGGCGTA TTTAGTGCAT TGCCACGACT TTTAGAACGT	6480
ACGGGAATGG GAGAAAAAGG CAGTATTACC GCATTTTATA CGGTACTGGT GGAAGGCGAT	6540
GATATGAATG AAGCCGTTGG CGGATGAAGT CCGTTCACTG CTTGATGGAC ATATTGTACT	6600
ATCCCGACGG CTTGCAGAGA GGGGGCATT TAATGCCATT GACGTGTTGG CAACGCTCAG	6660
CCGCGTTTTT CCAGTCGTTA CCAGCCATGA GCATCGTCAA CTGGCGGCGA TATTGCGACG	6720
GTGCCTGGCG CTTTACCAGG AGGTTGAACT GTTAATACGC ATTGGGGAAT ACCAGCGAGG	6780
AGTTGATACA GATACTGACA AAGCCATTGA TACCTATCCG GATATTTGCA CATTTTTCG	6840
ACAAAGTAAG GATGAAGTAT GCGGACCCGA GCTACTTATA GAAAAATTAC ACCAAATACT	6900
CACCGAGTGA TCATGGAAAC TTTGCTGGAG ATAATCGCGC GGCTGAAAAG CAATTACGCG	6960
GCAAGCTTAC CGTACTTGAT CAGCAGCAAC AGGCGATTAT TACGGAACAG CAGATTTGCC	7020
AGACGCGCGC TTTAGCAGTG TCTACCAGAC TGAAAGAATT AATGGGCTGG CAAGGTACGT	7080
TATCTTGTC A TTTATTGTTG GATAAGAAAC AACAAATGGC CGGGTTATTC ACTCAGGCGC	7140

AGAGCTTTTT	GACGCAACGG	CAAGCAGTTA	GAGAATCAGT	ATCAGCAGCT	TGTCTCCCGG	7200
CGAAGCGAAT	TACAGAAGAA	TTTTAATGCG	CTTATGAAAA	AGAAAAGAAAA	AATTACTATG	7260
GTATTAAGCG	ATGCGTATTA	CCAAAGTTGA	GGGAAGTCTT	GGGTTGCCAT	GCCAGTCTTA	7320
TCAGGATGAT	AACGAGGCGG	AGGCGGAACG	TATGGACTTT	GAACAACCTCA	TGCACCAGGC	7380
ATTACCCATT	GGTGAGAATA	ATCCTCCTGC	AGCATTGAAT	AAGAACGTGG	TTTTCACGCA	7440
ACGTTATCGT	GTTAGTGGCG	GTTATCTTGA	CGGTGTAGAG	TGTGAAGTAT	GTGAATCAGG	7500
GGGGCTAATC	CAGTTAAGAA	TCAATGTCCC	TCATCATGAA	ATTTACCGTT	CGATGAAAGC	7560
GCTAAAGCAG	TGGCTGGAGT	CTCAGTTGCT	GCATATGGGG	TATATAATTT	CCCTGGAGAT	7620
ATTCTATGTT	AAGAATAGCG	AATGAAGAGC	GTCCGTGGGT	GGAGATACTT	CCAACGCAAG	7680
GCGCTACCAT	TGGTGAGCTG	ACATTGAGTA	TGCAACAATA	TCCAGTACAG	CAAGGGACAT	7740
TATTTACCAT	AAATTATCAT	AATGAGCTGG	GTAGGGTGTG	GATTGCAGAA	CAATGCTGGC	7800
AGCGCTGGTG	TGAAGGGCTA	ATTGGCACCG	CTAATCGATC	GGCTATCGAT	CCTGAATTGC	7860
TATATGGAAT	AGCTGAATGG	GGGCTGGCGC	CGTTATTGCA	AGCCAGTGAT	GCAACCCTCT	7920
GTCAGAACGA	GCCGCCAACA	TCCTGCAGTA	ATCTACCACA	TCAGCTAGCG	TTGCATATTA	7980
AATGGACAGT	TGAAGAGCAT	GAGTTCCATA	GCATTATTTT	TACATGGCCA	ACGGGTTTTT	8040
TGCGCAATAT	AGTCGGAGAG	CTTTCTGCTG	AGCGACAACA	GATTTATCCT	CCCCCTCCTG	8100
TGGTAGTCCC	TGTATATTCA	GGCTGGTGCC	AGCTTACATT	AATCGAACTT	GAGTCTATCG	8160
AAATCGGCAT	GGGCGTTCGG	ATTCATTGCT	TCGGCGACAT	CAGACTCGGT	TTTTTTTGCTA	8220
TTCAACTACC	TGGGGGAATC	TACGCAAGGG	TGTTGCTGAC	AGAGGATAAC	ACGATGAAAT	8280
TTGACGAATT	AGTCCAGGAT	ATCGAAACGC	TACTTGCGTC	AGGGAGCCCA	ATGTCAAAGA	8340
GTGACGGAAC	GTCTTCAGTC	GAAC TTGAGC	AGATA CCACA	ACAGGTGCTC	TTTGAGGTCTG	8400
GACGTGCGAG	TCTGGAAATT	GGACAATTAC	GACA ACTTAA	AACGGGGGAC	GTTTTGCCTG	8460
TAGGTGGATG	TTTTGCGCCA	GAGGTGACGA	TAAGAGTAAA	TGACCGTATT	ATTGGGCAAG	8520
GTGAGTTGAT	TGCCTGTGGC	AATGAATTTA	TGGTGCGTAT	TACACGTTGG	TATCTTTGCA	8580
AAAATACAGC	GTAAACCTGA	TAAGAAAAAT	AATATGCGAA	CAATATAATA	GCGTTCCAGG	8640
TCGTGTCATG	AGAGATACAG	TATGTCTTTA	CCCGATT CGC	CTTTGCAACT	GATTGGTATA	8700
TTGTTTCTGC	TTTCAATACT	GCCTCTCATT	ATCGTCATGG	GAAC TTCITT	CCTTAAACTG	8760
GCGGTGGTAT	TTTCGATTTT	ACGAAATGCT	CTGGGTATT C	AACAAGTCCC	CCCAAATATC	8820

GCAC	TGTATG	GCCTT	GCCTT	TGTACTTT	TCC	TTATT	CATTA	TGGGG	CCGAC	GCTAT	TAGCT	8880
GTAAA	AAGAGC	GCTGG	CATCC	GGTTC	CAGGTC	GCTGG	CGCTC	CTTTCT	TGGAC	GTCTG	AGTGG	8940
GACAG	TAAAG	CATTAG	CGCC	TTATC	GACAG	TTTTT	TGCAAA	AAAAC	TCTGA	AGAGA	AAGGAA	9000
GCCA	ATTATT	TTCGGA	ATTT	GATAAA	ACGA	ACCTG	GGCCTG	AAGAC	ATAAA	AAGAA	AGATA	9060
AAAC	TGATT	CTTTG	CTCAT	ATTAAT	TCCG	GCATTT	TACGG	TGAGT	CAGTT	AACGC	CAGGCA	9120
TTTC	GGATTG	GATTAC	TTAT	TCTT	CCC	TTTCT	TGGCTA	TTGAC	CTGCT	TATTT	CAAAT	9180
ATACT	GCTGG	CTATG	GGGAT	GATGAT	GGTG	TCGCC	GATGA	CCATT	TTCATT	ACCGT	TTAAG	9240
CTGCT	AATAT	TTTTA	CTGGC	AGGCG	GTGG	GATCT	GACAC	TGGCG	CAATT	GGTAC	AGAGC	9300
TTTT	CATGAA	TGATT	CTGAA	TTGAC	GCAAT	TTGTA	ACGCA	ACTTTT	TATGG	ATCGT	CCTTT	9360
TTAC	GCTCTAT	GCCGG	TAGTG	TTGGT	TGGCAT	CGGTAG	TTGG	TGTCAT	CGTA	AGCCT	TGTTC	9420
AGGC	CTTGAC	TCAA	AATACAG	GACCA	AACGC	TACAG	TTTCAT	GATTAA	ATTA	TTGGC	AATTG	9480
CAATA	ACCTT	AATGG	TCAGC	TACCC	CATGGC	TTAGC	GGTAT	CCTGT	TGAAT	TATAC	CCGGC	9540
AGATA	AATGTT	ACGA	ATTGGA	GAGCAT	TGGTT	GAATG	GCACA	ACAGG	TAAAT	GAGTG	GCTTA	9600
TTGC	ATTGGC	TGTGG	CTTTT	ATTCG	ACCAT	TGAGC	CTTTC	TTTATT	ACTT	CCCTT	TATTAA	9660
AAAG	TGGCAG	TTTAG	GGGCC	GCAC	TTTTTAC	GTAAT	TGGCGT	GCTTAT	TGTCA	CTTAC	CTTTC	9720
CGATA	TTACC	AATCAT	TTTAC	CAGC	AAGA	TTATG	ATGCA	TATTG	GTAAA	GATTAC	AGTT	9780
GGTTA	GGGTT	AGTCA	CTGGA	GAGGT	GATTA	TTGGT	TTTTTC	AATTG	GGTTT	TGTGC	GGCGG	9840
TTCC	CTTTTG	GGCCG	TTGAT	ATGGC	GGGGT	TTCTG	CCTGA	TACTTT	TACGT	GGCGC	GACAA	9900
TGGG	TACGAT	ATTCA	ATTCT	ACAAT	AGAAG	CTGAA	ACCTC	ACTTTT	TGGC	TTGCT	TTTTCA	9960
GCCAG	TTCTT	GTGTG	TTATT	TTCTT	TATAA	GCGGC	GGCAT	GGAGT	TTATA	TTAA	ACATTC	10020
TGTAT	GAGTC	ATATC	AATAT	TTACC	ACCAG	GGCGT	ACTTT	ATTATT	TGAC	CAGCA	ATTTT	10080
TAAA	ATATAT	CCAGG	CAGAG	TGGAG	AACGC	TTTAT	CAATT	ATGTAT	CAGC	TTCTC	TCTTC	10140
CTGCC	CATAAT	ATGTAT	TGGTA	TTAGC	CGATC	TGGCT	TTAGG	TCTTTT	TAAAT	CGGTC	GGCAC	10200
AACA	ATTGAA	TGTGT	TTTTTC	TTCTC	AATGC	CGCTC	AAAAG	TATATT	TGGTT	CTACT	GACGY	10260
CCTG	ATCTCA	TTCC	CTTATG	CTCTT	CATCA	CTATT	TGGTT	GAAAG	CGATA	AATTT	TATAT	10320
TTATC	TAAAA	GACTG	GTTTC	CATCT	TGATG	AGCGA	GAAAA	CAGAA	CAGCC	TACAG	AAAAG	10380
AAATT	ACGTG	ATGGC	CGTAA	GGAAG	GGCAG	GTTGT	CAAAA	GTATT	GAAAT	AACAT	CATTA	10440
TTTC	AGCTGA	TTGCG	CTTTA	TTTGT	ATTTT	CATT	TCTTTA	CTGAA	AAGAT	GATTT	TGATA	10500
CTGAT	TGAGT	CAATA	ACTTT	CACAT	TACAA	TTAGT	TAAATA	AACC	ATTTTC	TTATG	CATTA	10560

ACGCAATTGA	GTCATGCTTT	AATAGAGTCA	CTGACTTCTG	CACTGCTGTT	TCTGGGCGCT	10620
GGGGTAATAG	TTGCTACTGT	GGGTAGCGTG	TTTCTTCAGG	TGGGGGTGGT	TATTGCCAGC	10680
AAGGCCATTG	GTTTTAAAAG	CGAGCATATA	AATCCGGTAA	GTAATTTTAA	GCAGATATTC	10740
TCTTTACATA	GCGTAGTAGA	ATTATGTAAA	TCCAGCCTAA	AAGTTATCAT	GCTATCTCTT	10800
ATCTTTGCCT	TTTTCTTTTA	TTATTATGCC	AGTACTTTTC	GGGCGCTACC	GTACTGTGGG	10860
TTAGCCTGTG	GCGTGCTTGT	GGTTTCTTCT	TTAATAAAAT	GGTTATGGGT	AGGGGTGATG	10920
GTTTTTTTATA	TCGTCGTTGG	CATACTGGAC	TATTCTTTTC	AATATTATAA	GATTAGAAAA	10980
GCTATCTAAA	AATGAGTAAA	GATGACGTAA	AACAGGAGCA	TAAAGATCTG	GAGGGCGACC	11040
CTCAAATGAA	GACGCGGCGT	CGGAAATGCA	GAGTGAAATA	CAAAGTGGGA	GTTTAGCTCA	11100
ATCTGTTAAA	CAATCTGTTG	CGGTAGTGCG	TAATCCAACG	CATATTGCGG	TTTGTCTTGG	11160
CTATCATCCC	ACCGATATGC	CAATACCACG	CGTCCTGGAA	AAAGGCAGTG	ATGCTCAAGC	11220
TAACTATATT	GTTAACATCG	CTGAACGCAA	CTGCATCCCC	GTTGTTGAAA	ATGTTGAGCT	11280
GGCCCGCTCA	TTATTTTTTG	AAGTGGAAACG	CGGAGATAAA	ATTCTTGAAA	CGTTATTTGA	11340
ACCCGTTGCA	GCCTTGTTAC	GTATGGTGAT	GAAGATAGAT	TATGCGCATT	CTACCGAAAC	11400
ACCATAAATG	CTTTTGGTAT	GCTTCTTCAG	GCCACTGCGA	AGGTTAAGAG	GGTAATAGCG	11460
TATAGAGCAG	TGCTTGACGA	TAAAGGTGAG	AGACTGAAAA	TAATCGCTTT	TAGCCTGGCA	11520
CAAGCACCAG	ATAGCGTATT	ATAAAATTAA	ACAAGATAAT	GGATTGGTGC	GTCTGAATGG	11580
ACTCGAACCA	CTCGACCCCC	ACCATGTCAA	GGTGGTGCTC	TAACCAACTG	AGCTATGAAC	11640
GGCAACGTTG	TAGGTGACAA	CGGGGACGAA	TATTAGCGTC	ACAACCGCAA	TGAGGCAAGA	11700
GGGAAATCGC	AATTTTCTTC	CTGAAATCAC	CTGATTGCGG	TGGAAATATG	CAACATGTCTG	11760
AGAAAATAGC	CGCCATGCGA	CGGCTATCGT	CGTATTATCG	GAGCGCGCTG	CAAAATGATG	11820
GCGGACGGCT	GACGTTGTAG	ATAGCGCATC	CGTAGCATCA	TTAACACCGC	CGCCGAGGTC	11880
AGGCCGATGA	TGAACCCCAT	CCAGAAGCCT	GCCGGTCCCA	TACGATCCAC	CACCAAATCC	11940
GTTAACGCCA	GGATATAACC	GCTGGGTAAA	CCTAACACCC	AGTAGGCGGT	AAAGGTGATA	12000
AAAAAGATGG	AACGCGTATC	TTTATAACCG	CGCAGAATAC	CGCTGCCGAT	AACCTGTATA	12060
GAGTCGGAAA	TCTGGTAAAC	CGCAGCGAGC	AGCATTAATT	GCGGCAAGCG	CCACGACCTC	12120
AGGGTTGTCA	TTGTAGAGCA	AAGCAATATG	CTTACGCAGA	GTAACGGTAA	AAATAGCGGT	12180
AACCACAGCC	ATACAAATGC	CGACGCCTAA	ACCGGTACGC	GCTGCGTTTG	CGCATCCAGC	12240

GTTGAGCCCT GGCCAGACC GATAACCCAC TCGAATCGTT ACCGCCGCAG CCAGCGACAT 12300
 CGGCAGTACG AACATCAGCG AGCTAAAGTT AAGCGCAATC TGATGACCGG CGACATCCAC 12360
 AATACCTAAT GGCAGAACCA GCAGCGCAAC GACCGCAAAT AACGTCACCTT CAAAGAACAG 12420
 CCAGCGCAAT CGGCAACCCC AGTTGAATCA GCGCTTCAT GACGACGCTA TCGGGTTTGC 12480
 CAAAGCCTTT TTCATTACGA ATATCAGCGA TTGAACGCGC GTGTTTAATG TAAGAAAGCA 12540
 TGGCGATAAA CATCACCCAA TAGACCGCCG CAGTCGCAAC GCCGCAGCCG ATACCGCCGA 12600
 GTTCCGGCAT ACCAAAATGG CCATAGATAA AAATATAGTT CACCGGAATA TTCACCAGCA 12660
 GGCCCAAAAA TCCCATCACC ATACCCGGTT TGGTTTTGGC CAGACCTTCG CACTGGTTTC 12720
 GCGCTACCTG AAAGAAAAGG TATCCTGCGC CCCACAGCAG CGCGCAAGA TAACCCACGG 12780
 CTTTATCGGC CAGCGCCGGA TCAATATTAT GCATAGAGCG GATAATGTAT CCGGCATTCC 12840
 ACAGGACGAT CATCACCAGC ACGGAGACAA AGCCCGCCAG CCAGAACCCT TGTCGAACCT 12900
 GATGCGCGAT ACGCTCACGA CGGCCGGAGC CATTGAGTTG CGCAATCACA GCGTCAAGG 12960
 CCAGCAGTAA GCCGTGACCA AACAAAATGG CGGGAAGCAG ATAGAGGTGC CGATAGCGAC 13020
 GGCAGCCATG TCCGTAGCGC TATAGCCTCC CGCCATGACG GTATCGACGA ATCCATTGCG 13080
 GTCTATACCA CTGCGCAAG GATCACCGGT ATCTGAACGC TAATAACTGA CGCGCTTCAC 13140
 TGGTATACTT CTGCACGTAT TCACCTTTTA TTTTGTGTGTT ATATGAAAGA CTA AAAAGCC 13200
 GCCGAAGTGG CAGCCAAAAG AAATAGCAGG GGAAATTTCA GTCTATTGTA GCGGGGTATT 13260
 ACTATTTCTC CAGTGAAAAA ACAGTTGTTA ACGGCGCATT GCTGGCAAGC TGTTTTTCCA 13320
 CCTGCTATTG TGCTGAACAG TTCTGCTTTT ATTTATTTCA GGAGTTGAAG ATATGTTTAC 13380
 GGGGATCGTA CAGGGTACCG CGAACTGGT ATCGATA 13417

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5746 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: DNA sequence of VGC II cluster C

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGATCCTTTT TCTTTAATGC TGCTAACGTT TCTTGCAAAA TGCGTTGATG AGATTCATCC 60
 AGTACACCAC TGATAACAAA AGAGCGNCGC ATTGGCNWAM MWTKRNNMRN NSCNNNACTA 120

AACCGTTCTC TATTATCGCA GAAATAATAT CATCCCCCTG AGACTGATGA GAGTGACTAA	180
TCTGCCAGTG CAATAACCCG GGAATATCTG CAAGTAATGG TTGAACCTTG CGCCATTGCT	240
GATCCATTTG TATATCATCA TGAATTAACA CGCTCCCCGG CCCTTCGCTG GATACTTCAG	300
CATNSSGGTA ACCCATTTTT ATCAAAACAT CCTGCACTTC TCGTACCAAT AAGTCATCAC	360
AGATTACACC ATCCCGATAC ATGACCCCCC ATGATTTCGAG AGTCGCTCTC ACCTTTTGCA	420
TCTGTTGCTG TGACGAGCAA TAACCGGACA ACTGCAGGCT GCCATCTTCT TTCCATTGCG	480
CCCGCACATA ATGAATATTG CTTTGTGCTA ATAAAACTT AACCCGCAAA GGTAAGTCAT	540
TTACCGTTTC AGGCTGACCA CTAATACTTA ACAGGACACC CATTCCACCG ATGAAAATCA	600
AGAATACGCC AGCCAACCAC CAGTACCCTG ATCTGGAAAC GGGTATTTGA TAATCAGCAA	660
GTTCAACAATC CTGTTTACCA AACGCGATAS SCACTCCCGC AACCTGCAAA ACCCCACTGG	720
ATGGTAGCGG CTTATTTGGA TTAAATCTGC GGCCATTAAC TCTAACTCTG GCTTTCCCGG	780
CATCAACAAA TAAACTATCT GCCTGTTCTC TCAGAATAAT TTTTTCATTT ATAGCCAGCG	840
AATACAAATA TCGCATCCCT TCTCCCCCAG TGACAGGTTA CCTTCATTCA GCCATACTTC	900
CCGGCCTTGT AAAACGTGAC CTAAAAAAGC TATTTTCCAG GAACTCTTTG GATTAACCAT	960
GAGATATGCC ATTATTTACT ACTGAGGCTT TAATCAAAAA AAGCCTGATT ACACTATGTA	1020
CTTGAGTCGT ATCATTGCGA AACAAATGAC CTACAACAGG AATATCGCCC AATAAAGGGA	1080
TTTTGTTTTG CGAGTGGATT TGTTTACCTT GTTTAAACCC TCCCAGCAAT NAGACTTTGC	1140
CCGGCCAATA ATGTGGCTTG CGAANCRATT TCAGAATTTT GCACTTCGGG CAGCGGGTCT	1200
GTNTYGCYTT KGNSTATCAC TTTGTTGTCC ATCCTGAANT ATTAAGATTA AGCATTATTT	1260
TTTGCGTGCC ATTGTCATTT AACAAAGCGAG GTGTAACGCG WNAACAAAGA ACCCGTAGTG	1320
ATGGATTCAA GTTTAGCCAC TTTTCTCCC TGCAGTTTGG TATAGAAAGT AATATTTTAA	1380
TCCAGCACAG CCTGGATATT ATTTAAAGTC ACCACAGATG GCTGGGAAAG TACATAAGCC	1440
TGAGAGCTTT TTTCCAGGGC ATTCAGACGC ACCATAAAGT TTGAGGTATC GCTGATTACC	1500
GTTGANNAAC CACTAGCACC ACCGTCATTC AAACCTGTAT TGAACGCAAT TTTCTTGCCA	1560
CCCAGCGACA CTGCCGTTCC CCAGTCGATG CCTAACTGGT TAATATCTCC AGCATTAACA	1620
TCGATAATTT TCACCGAAAT CTCTATCATC TGCTGGCGTT GATCTAATTC TGTGATGAGT	1680
TTCCGATACN NNGCCATATT GGNNNCATAA TCACGAACGA TCACTGCATT CTGGCGTNGG	1740
GTCGGCAGCA AACATNGGCA ATGCCTGTGT AGCGGGTGAA CCATTGTTCN TCGATGACGT	1800

CGGGACGCTG	GTTTTACTCA	TCTCACGCAA	TACACTAACG	ACCCCTGGNN	AACCACGACG	1860
GACTGATCGC	GATATTGGTA	CTGGGTATCC	ATCGCAGTGG	CATACTTAAG	CGTGTATATA	1920
CTTACACTCA	CCGCACTGTC	TTTTCGTTTG	ATTAACGCAT	TATCCAGCAC	TGAAGCTAAT	1980
TGACTAATAC	GAGTCAGGCA	GCTGGGAACA	CCGCTCACCT	CCACAGCTTT	GGTACCGGTA	2040
ATTTCTTTAA	CCTCGCATCC	CGGTGATGAA	AGGATATTCT	GGCTGCGTAA	GTAATGAATG	2100
AACCGTCCAG	TAGATAAAAT	ATTGAAAAGTG	ATAACCTGAT	GTTTTAATAA	CGATGCAGGA	2160
TATACATATA	ACATGCTGCC	ATCAAACCAG	GTAAGCAAAT	CATATTGTGC	TGCCAGGTTA	2220
TTCAAATAT	CGACCGGTGG	TCCAGGCGGA	ATTTTCCAC	TAAATGTAGC	TGTTATCAAT	2280
GGGCTAATAG	TAATAGCCGT	ATCATAGTTC	TCTGAGAGCA	GATGTNAAAA	CCTCTGCTAA	2340
TGGCATTGT	CTGGCATAAA	GGGTGAAGTC	ATTACCTTTC	CATGATAACT	CATCACTCTT	2400
TGCTGTATTG	AGTATAAATA	GTAAAATTAA	GATTAAACGT	TTATTTACTA	CCATTTTATA	2460
CCCCACCCGA	ATAAAGTTTA	TGGTGATTGC	GTATTACATT	TTTTNAAAAT	GCAAGTTAAA	2520
GCCAGGTGTT	TTTCTATCTC	AATAGCAATA	AGCTCAGAGC	TACTACTTGT	GGTATAATAA	2580
CCGTTTAACC	ATCCCCCATC	CGCTGTGAGC	TGTATAGCAT	AATCATGGAC	GTCCGGGTGT	2640
GCGCAARCRG	TAGTGTCAMM	TAGGCAAGAC	AAGGCTTAGG	TAAGCTTTCC	AGGTCATTTA	2700
AGAACAAAGA	AATAGAAAAT	GCTTCTGAGA	AAATTTCTYC	YBHNNNNNNN	NNNNNNNNNN	2760
NNNNNNNNCA	TCAATAGTCA	TTATCCAGGA	TSSKMTWWYM	NYKSSSCYS	WKATMYYSWR	2820
WWTTAATGGA	ATGCCTTTTA	AACTGCCAG	CATGAATCCC	TCCTCAGACA	TAAATGGGAG	2880
TTTCTATCAA	ATTCGCTCAC	AACCACATCC	GTAAAAAGCC	TGATTACAT	TTATTTGAC	2940
TATACTCTTC	TTGTACAATA	TCAGGATGCT	GTCTACATAT	ACCTTGTCAC	AGGCGATTCT	3000
ATCATTCGGA	TTTTCCGATA	AATTNMMCAA	TTACATTTTC	AGCATTGACA	TAAAACTTA	3060
CAATTTGNAA	AATTATTTAT	TAAATAAACT	GTTACGATGT	TTTTACATCG	CCATCTTATT	3120
AAAAAGTAAT	TGTAGTCATC	GACTNGGTTA	TATATGAAGA	AATTTATCTT	CCTAATGATA	3180
ACACCATCGA	TTAATCWWCT	GATGAAACTA	TATGTACTGC	GATAGTGATC	AAGTGCCAAA	3240
GATTTTGCAA	CAGGCAACTG	GAGGGAAGCA	TTATGAATTT	SSTCAATCTC	AAGAATACSS	3300
YSYRNNNNNN	TCTTTAGTAA	TCAGGCTAAC	TTTTTTATTT	TTATTAACAA	CAATAATTWT	3360
TTGGCTGCTA	TCTGTGCTTA	CCGCAGCTTA	TATATCAATG	GTTTCRGAAC	GGCAGCATAT	3420
AATAGAGGAT	TTATCCGTTC	TATCCGAGAT	GAATATTGTA	CTAAGCAATC	AACGGTTTGA	3480
AGAAGCTGAA	CGTGACGCTA	AAAATTTAAT	GATCAATGC	TCATTAGCGA	CTGAGATTCA	3540

TCATAACGAT	ATTTTCCCTG	AGGTGAGCCG	GCATCTATCT	GTCGGTCCTT	CAAATTGCAC	3600
MGCCGACGCT	NAACGGAGAG	AAGCACCGTC	TCTTTCTGCA	GTCCTCTGAT	ATCGATGAAA	3660
ATAGCTTTTCG	TCGCGATAGT	TTTATTCTTA	ATCATAAAAA	TGAGATTTTCG	TTATTATCTA	3720
CTGATAACCC	TTCAGATTAT	TCAACTCTAC	AGCCTTTAAC	GCGAAAAAGC	TTTCCTTTAT	3780
ACCCAACCCA	TGCCGGGTTT	TACTGGAGTG	AACCAGAATA	CATAAACGGC	AAAGGATGGC	3840
AACGCTTCCG	TTGCGGTTGC	CGATCAGGCA	AGGCGTATTT	TTTGAGGTGA	CGGTTAAACT	3900
TCCCGATCTC	ATTACTAAGA	GCCACCTGCC	ATTAGATGAT	AGTATTCGAG	TATGGCTGGA	3960
TCAAAACAAC	CACTTATTGC	CGTTTTTATA	CATCCCGGCA	AAAAATACGT	ACACAGTTAG	4020
AAAATGTAAC	GCTGCATGAT	GGATGGCAGC	AAATTCCCGG	ATTTCTGATA	TTACGCACAA	4080
CCTTGCAATG	CCCCGGATGG	AGTCTGGTTA	CGCTGTACCC	ATACGGTAAT	CTACATAATC	4140
GCATCTTAAA	AATTATCCTT	CAACAAATCC	CCTTTACATT	AACAGCATTG	GTGTTGATGA	4200
CGTCGGCTTT	TTGCTGGTTA	CTACATCGCT	CACTGGCCAA	ACCGTTATGG	CGTTTTGTCTG	4260
ATGTCATTAA	TAAAACCGCA	ACTGCACCGC	TGAGCACACG	TTTACCAGCA	CAACGACTGG	4320
ATGAATTAGA	TAGTATTGCC	GGTGCTTTTA	ACCAACTGCT	TGATACTCTA	CAAGTCCAAT	4380
ACGACAATCT	GGAAAACAAA	GTCGCAGACG	CACCCAGGCG	CTAATGAAG	CAAAAAACG	4440
CGCTGAGCNA	GCTAACAAAC	GTAAAAGCAT	TCATCTTACG	GTAATAAGTC	ATGAGTTACG	4500
TACTCCGATG	AATGGCGTAC	TCGGTGCAAT	TGAATTATTA	CAAACCACCC	CTTTAAACAT	4560
AGAGCAACAA	GGATTAGCTG	ATACCGCCAG	AAATTGTACA	CTGTCTTTGT	TAGCTATTAT	4620
TAATAATCTG	CTGGATTTTT	CACGCATCGA	GTCTGGTCAT	TTACACATTAC	ATATGGAAGA	4680
AACAGCGTTA	CTGCCGTTAC	TGGACCAGGC	AATGCAAACC	ATCCAGGGGC	CAGCGCNAAA	4740
GCAAAAAACT	GTCATTACGT	ACTTTTGTCG	GTCAACATGT	CCCTCTCTAT	TTTCATACCG	4800
ACAGTATCCG	TTTACNNCAA	ATTTTGTTTA	ATTTACTCGG	GAACGCGGTA	AAATTTACCG	4860
AAACCGGAGG	ATACGTCTGA	CGGTCAAGCG	TCATGAGGAA	CAATTAATAT	TTCTGGTTAG	4920
CGATAGCGGT	AAAGGGATTG	AAATACAGCA	GCAGTCTCAA	ATCTTTACTG	CTTTTTATCA	4980
AGCAGACACA	AATTCGCAAG	GTACAGGAAT	TGGACTGACT	ATTGCGTCAA	GCCTGGCTAA	5040
AATGATGGGC	GGTAATCTGA	CACTAAAAAG	TGTCCCCGGG	GTGGAACCT	GTGTCTCGCT	5100
AGTATTACCC	TTACAAGAAT	ACCAGCCGCC	TCAACCAATT	AAAGGGACGC	TGTCAGNNNC	5160
CGTTCTGCCT	GCATCGGCAA	CTGGCTTGCT	GGGGAATACG	CGGTGAACCA	CCCCACCAGC	5220

AAAATGCGCT TCTCAANN CN AGAGCTTTTG TATTTCTCCG GAAAACTCTA CGACCTGGCG 5280
 CAACAGTTAA TATTGTGTAC ACCAAATATG CCAGTAATAA ATAATTTGTT ACCACCCTGG 5340
 CAGTTGCAGA TTCTTTTGGT TGATGATGCC GATATTAATC GGGATATCAT CGGCAAAATG 5400
 CTTGTCAGCC TGGGCCAACA CGTCACTATT GCCGCCAGTA GTAACGAGGC TCTGACTTTA 5460
 TCACAACAGC AGCGATTCTGA TTTAGTACTG ATTGACATTA GAATGCCAGA AATAGATGGT 5520
 ATTGAATGTG TACGATTATG GCATGATGAG CCGAATAATT TAGATCCTGA CTGCATGTTT 5580
 GTGGCACTAT CCGCTAGCGT ASCVNMAGAW RWTMWTCTY GTDDAAAAAA WRDGRKDHWT 5640
 CATHAYANNT TACAAAACCA GTGACATTGG CTACCTTAGC TCGCTACATC AGTATTGCCG 5700
 CAGAATACCA ACTTTTACGA AATATAGAGC TACAGGAGCA GGATCC 5746

(2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CCACCAGCCG CTGGGGTACC AGGGCCAGGC GACGGATATT GAAATTCACG CCCGCGAAAT 60
 TTTGAAAGTA AAAGGGCGCA TGAATGAACT TATGRMKYKM MATACGGGTC ANTCTCTTGA 120
 GCAGATTGAA SGTGATACTG A 141

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TGAAGCGGTA GAGTACGGTT TGGTTGACTC AATTTTGACC CATCGTAATT GATGCCCTGG 60
 ACGCAA 66

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CCAACCGTTG GCGGGCTACC AGGGCCAGGC GACCGATATC GAAATTCATG CCCGTGAAAT	60
TCTGAAAGTT AAAGGGCGCA TGAATGAACT TATGGCGCTT CATACGGGTC AATCATTAGA	120
ACAGATTGAA CGTGATACCG A	141

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGAAGCGGTG GAATACGGTC TGGTCGATTC GATTCTGACC CATCGTAATT GATGCCAGAG	60
GCGCAA	66

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GATATCGAAA TTCATGCCCG TGAAATTCTG AAAGTTAAAG GGCGCATGAA TGAACCTATG	60
GCGCTTCATA CGGGTCAATC ATTAGAACAG ATTGAACGTG ATACCGA	107

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

TGAAGCGGTG GAATACGGTC TGGTCGATTC GATTCTGACC CATCGTAATT GATGCCAGAG	60
---	----

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Ser Ile Ile Leu Pro Glu Tyr His Gly Ala Ala Cys Gln Ala Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:49:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

(2) INFORMATION FOR SEQ ID NO:50:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Phe Ile Ala His Cys Gln Lys Met Lys Arg Ile Lys Cys Trp His Tyr
20 25 30

Leu Cys Ser Ile Ile Leu Met Arg Lys Lys Thr Gly Arg Gly Trp Cys
35 40 45

Asn Leu Thr Cys Arg Ala Val Gly Ser Leu Leu Met Arg Leu Arg Leu
50 55 60

Leu Arg Leu Asn Gly Tyr Pro His Arg Ala Val Tyr Asn Gly Gly
65 70 75

(2) INFORMATION FOR SEQ ID NO:51:

(ii) MOLECULE TYPE: protein

1. $\frac{1}{2}$ 2. $\frac{1}{2}$ 3. $\frac{1}{2}$ 4. $\frac{1}{2}$ 5. $\frac{1}{2}$ 6. $\frac{1}{2}$ 7. $\frac{1}{2}$ 8. $\frac{1}{2}$ 9. $\frac{1}{2}$ 10. $\frac{1}{2}$ 11. $\frac{1}{2}$ 12. $\frac{1}{2}$ 13. $\frac{1}{2}$ 14. $\frac{1}{2}$ 15. $\frac{1}{2}$ 16. $\frac{1}{2}$ 17. $\frac{1}{2}$ 18. $\frac{1}{2}$ 19. $\frac{1}{2}$ 20. $\frac{1}{2}$ 21. $\frac{1}{2}$ 22. $\frac{1}{2}$ 23. $\frac{1}{2}$ 24. $\frac{1}{2}$ 25. $\frac{1}{2}$ 26. $\frac{1}{2}$ 27. $\frac{1}{2}$ 28. $\frac{1}{2}$ 29. $\frac{1}{2}$ 30. $\frac{1}{2}$ 31. $\frac{1}{2}$ 32. $\frac{1}{2}$ 33. $\frac{1}{2}$ 34. $\frac{1}{2}$ 35. $\frac{1}{2}$ 36. $\frac{1}{2}$ 37. $\frac{1}{2}$ 38. $\frac{1}{2}$ 39. $\frac{1}{2}$ 40. $\frac{1}{2}$ 41. $\frac{1}{2}$ 42. $\frac{1}{2}$ 43. $\frac{1}{2}$ 44. $\frac{1}{2}$ 45. $\frac{1}{2}$ 46. $\frac{1}{2}$ 47. $\frac{1}{2}$ 48. $\frac{1}{2}$ 49. $\frac{1}{2}$ 50. $\frac{1}{2}$ 51. $\frac{1}{2}$ 52. $\frac{1}{2}$ 53. $\frac{1}{2}$ 54. $\frac{1}{2}$ 55. $\frac{1}{2}$ 56. $\frac{1}{2}$ 57. $\frac{1}{2}$ 58. $\frac{1}{2}$ 59. $\frac{1}{2}$ 60. $\frac{1}{2}$ 61. $\frac{1}{2}$ 62. $\frac{1}{2}$ 63. $\frac{1}{2}$ 64. $\frac{1}{2}$ 65. $\frac{1}{2}$ 66. $\frac{1}{2}$ 67. $\frac{1}{2}$ 68. $\frac{1}{2}$ 69. $\frac{1}{2}$ 70. $\frac{1}{2}$ 71. $\frac{1}{2}$ 72. $\frac{1}{2}$ 73. $\frac{1}{2}$ 74. $\frac{1}{2}$ 75. $\frac{1}{2}$ 76. $\frac{1}{2}$ 77. $\frac{1}{2}$ 78. $\frac{1}{2}$ 79. $\frac{1}{2}$ 80. $\frac{1}{2}$ 81. $\frac{1}{2}$ 82. $\frac{1}{2}$ 83. $\frac{1}{2}$ 84. $\frac{1}{2}$ 85. $\frac{1}{2}$ 86. $\frac{1}{2}$ 87. $\frac{1}{2}$ 88. $\frac{1}{2}$ 89. $\frac{1}{2}$ 90. $\frac{1}{2}$ 91. $\frac{1}{2}$ 92. $\frac{1}{2}$ 93. $\frac{1}{2}$ 94. $\frac{1}{2}$ 95. $\frac{1}{2}$ 96. $\frac{1}{2}$ 97. $\frac{1}{2}$ 98. $\frac{1}{2}$ 99. $\frac{1}{2}$ 100. $\frac{1}{2}$

1

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

1

5

10

15

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

1

5

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

1

5

10

15

(i) SEQUENCE CHARACTERISTICS:

- (C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Arg Phe Ser Glu Leu Ser Cys Arg Ile Tyr Lys Ile Phe Thr Ser Gly
1 5 10 15

Gln Tyr Gly Gly Leu Ser Gly Lys Asn
20 25

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Phe Asn Arg Asp Val Asn Pro Trp Val Ala Ile Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Leu Asp Ala Ala Cys
1 5

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Ile Gln Asn Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Arg Thr Arg Glu Thr Asn Ile Leu Asp Tyr Gly Arg Tyr Gln Arg Gln
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg Glu Gly Gly Glu Val Val Asp Glu Ile Pro Leu Ser Val Asp Val
1 5 10 15

Ile Val Asp Arg Thr Val Ile Arg Ser Gly His Pro Asp Arg Leu Phe
20 25 30

Leu Pro Glu Thr Pro Phe Leu Ser Arg Pro Asp Pro Glu Val Leu Gln
35 40 45

Leu Tyr Arg Tyr Phe Trp Gln Pro Ala Arg Tyr Ala Val Pro Glu Trp
50 55 60

Leu Asp Lys Leu Gly Phe His Leu Gln Thr Ala Gly Val Met Ala Ile
65 70 75 80

Gly Pro Ser Trp Ile Val Phe Leu Thr Glu Arg
85 90

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Glu Glu Ala Leu Leu Phe Gln Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

[illegible]

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

[illegible]

(2) INFORMATION FOR SEQ ID NO:64:

```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 6 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Val Leu Leu His Phe Leu
1 5

1000 900 800 700 600 500 400 300 200 100 0

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

Arg Ala Cys Val Lys Ile Arg Trp Lys Lys Trp Lys Trp Asn Gly Trp
 1 5 10 15

Asn Ser Met

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Ile Tyr Lys Thr Met Lys Ile Asn Phe Val His Trp Ser Ile Thr
 1 5 10 15

Gln Arg Ile Ile Leu Lys Ile Val
 20

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asn Arg Phe Cys Trp Pro Gly Ser Thr Asn Ser Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Thr Val Leu Cys Ala Ile Val Trp His Ala Arg Pro Arg Leu Trp Arg
 1 5 10 15

Lys Arg Glu Arg Phe Ile Cys Val Phe Ile Leu Lys Lys Arg His
 20 25 30

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

(2) INFORMATION FOR SEQ ID NO:73:

(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Ser Ser Leu Val Ser Leu Pro Ile Arg Leu Asn Phe Pro Gln His
1 5 10 15

Asp Met Pro Leu Asn Phe His Phe Leu Val Ile Ser Thr Arg Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Gly Tyr Val Met Val Lys Ile Lys Glu Val Ala Met Asn Ile Lys
1 5 10 15

Ile Asn Glu Ile Lys Met Thr Pro Pro Thr Ala Phe Thr Pro Gly Gln
20 25 30

Val Ile Glu Glu Gln Glu Val Ile Ser Pro Ser Met Leu Ala Leu Gln
35 40 45

Glu Leu Gln Glu Thr Thr Gly Ala Ala Leu Tyr Glu Thr Met Glu Glu
50 55 60

Ile Gly Met Ala Leu Ser Gly Lys Leu Arg Glu Asn Tyr Lys Phe Thr
65 70 75 80

Asp Ala Glu Lys Leu Glu Arg Arg Gln Gln Ala Leu Leu Arg Leu Ile
85 90 95

Lys Gln Ile Gln Glu Asp Asn Gly Ala Thr Leu Arg Pro Leu Thr Glu
100 105 110

Glu Asn Ser Asp Pro Asp Leu Gln Asn Ala Tyr Gln Ile Ile Ala Leu
115 120 125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

His Met His Arg Thr Leu Gly Ala Lys Ser Phe Gly Arg Ser Ile Ser
1 5 10 15

Thr Phe Ala Ser Phe Ala Val Ile Pro Trp Pro
20 25

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Lys Arg Val Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Gly Val Asp Leu Pro Val Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Tyr Ile Thr Ala Ala Thr Thr Arg Tyr Tyr Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Ala Leu Ala Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Tyr Arg Tyr Ser Phe Phe Ile Glu Asp Val Gln Ser Val Thr Pro
1 5 10 15

Thr Thr

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Cys Ala Val Tyr Ala Asp Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Arg Arg Arg Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Thr Asn Ser Arg Asn Ala Ser
1 5

- (2) INFORMATION FOR SEQ ID NO:86:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser Lys Asp Lys Ser Gly Phe Ile Leu Ile Pro Gly Phe Gln Tyr Leu
1 5 10 15

Gly Lys Leu Ala Phe Trp Leu Ile Met Arg Arg Gln Asp Gly Leu Gly
20 25 30

Ser His Tyr
35

- (2) INFORMATION FOR SEQ ID NO:87:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Tyr Ser Ala Phe Tyr Ser Ile Ser Arg Ile Ser
1 5 10

- (2) INFORMATION FOR SEQ ID NO:88:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Ala Phe Ser Asn Gln Tyr Val Leu Ala Ala Arg Thr Ile
1 5 10

- (2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 759 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

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Asn Tyr His Asn Gly Arg Ile Leu Leu Cys Gln Ile Leu Lys Gln Thr
 1              5              10              15

Phe Leu Asp Glu Glu Leu Leu Phe Lys Ala Leu Ala Asn Trp Lys Pro
      20              25              30

Ala Ala Phe Gln Gly Ile Pro Gln Arg Leu Phe Leu Leu Arg Asp Gly
      35              40              45

Leu Ala Met Ser Cys Ser Pro Pro Leu Ser Ser Ser Ala Glu Leu Trp
      50              55              60

Leu Arg Leu His His Arg Gln Ile Lys Phe Xaa Gly Val Ala Met Arg
      65              70              75              80

Ser Trp Leu Gly Glu Gly Val Arg Ala Gln Gln Trp Leu Ser Val Cys
      85              90              95

Ala Gly Arg Gln Asp Met Val Leu Ala Thr Val Leu Leu Ile Ala Ile
      100             105             110

Val Met Met Leu Leu Pro Leu Pro Thr Trp Met Val Asp Ile Leu Ile
      115             120             125

Thr Ile Asn Leu Met Phe Ser Val Ile Leu Leu Leu Ile Ala Ile Tyr
      130             135             140

Leu Ser Asp Pro Leu Asp Leu Ser Val Phe Pro Ser Leu Leu Leu Ile
      145             150             155             160

Thr Thr Leu Tyr Arg Leu Ser Leu Thr Ile Ser Thr Ser Arg Leu Val
      165             170             175

Leu Leu Gln His Asn Ala Gly Asn Ile Val Asp Ala Phe Gly Lys Phe
      180             185             190

Val Val Gly Gly Asn Leu Thr Val Gly Leu Val Val Phe Thr Ile Ile
      195             200             205

Thr Ile Val Gln Phe Ile Val Ile Thr Lys Gly Ile Glu Arg Val Ala
      210             215             220

Glu Val Ser Ala Arg Phe Ser Leu Asp Gly Met Pro Gly Lys Gln Met
      225             230             235             240

Ser Ile Asp Gly Asp Leu Arg Ala Gly Val Ile Asp Ala Asp His Ala
      245             250             255

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Arg Thr Leu Arg Gln His Val Gln Gln Glu Ser Arg Phe Leu Gly Ala
260 265 270

Met Asp Gly Ala Met Lys Phe Val Lys Gly Asp Thr Ile Ala Gly Ile
275 280 285

Ile Val Val Leu Val Asn Ile Ile Gly Gly Ile Ile Ile Ala Ile Val
290 295 300

Gln Tyr Asp Met Ser Met Ser Glu Ala Val His Thr Tyr Ser Val Leu
305 310 315 320

Ser Ile Gly Asp Gly Leu Cys Gly Gln Ile Pro Ser Leu Leu Ile Ser
325 330 335

Leu Ser Ala Gly Ile Ile Val Thr Arg Val Pro Gly Glu Lys Arg Gln
340 345 350

Asn Leu Ala Thr Glu Leu Ser Ser Gln Ile Ala Arg Gln Pro Gln Ser
355 360 365

Leu Ile Leu Thr Ala Val Val Leu Met Leu Leu Ala Leu Ile Pro Gly
370 375 380

Phe Pro Phe Ile Thr Leu Ala Phe Phe Ser Ala Leu Leu Ala Leu Pro
385 390 395 400

Ile Ile Leu Ile Arg Arg Lys Lys Ser Val Val Ser Ala Asn Gly Val
405 410 415

Glu Ala Pro Glu Lys Asp Ser Met Val Pro Gly Ala Cys Pro Leu Ile
420 425 430

Leu Arg Leu Ser Pro Thr Leu His Ser Ala Asp Leu Ile Arg Asp Ile
435 440 445

Asp Ala Met Arg Trp Phe Leu Phe Glu Asp Thr Gly Val Pro Leu Pro
450 455 460

Glu Val Asn Ile Glu Val Leu Pro Glu Pro Thr Glu Lys Leu Thr Val
465 470 475 480

Leu Leu Tyr Gln Glu Pro Val Phe Ser Leu Ser Ile Pro Ala Gln Ala
485 490 495

Asp Tyr Leu Leu Ile Gly Ala Asp Ala Ser Val Val Gly Asp Ser Gln
500 505 510

Thr Leu Pro Asn Gly Met Gly Gln Ile Cys Trp Leu Thr Lys Asp Met
515 520 525

Ala His Lys Ala Gln Gly Phe Gly Leu Asp Val Phe Ala Gly Ser Gln
530 535 540

Arg Ile Ser Ala Leu Leu Lys Cys Val Leu Leu Arg His Met Gly Glu
545 550 555 560

Phe Ile Gly Val Gln Glu Thr Arg Tyr Leu Met Asn Ala Met Glu Lys
565 570 575

Asn Tyr Ser Glu Leu Val Lys Glu Leu Gln Arg Gln Leu Pro Ile Asn
580 585 590

Lys Ile Ala Glu Thr Leu Gln Arg Leu Val Ser Glu Arg Val Ser Ile
595 600 605

Arg Asp Leu Arg Leu Ile Phe Gly Thr Leu Ile Asp Trp Ala Pro Arg
610 615 620

Glu Lys Asp Val Leu Met Leu Thr Glu Tyr Val Arg Ile Ala Leu Arg
625 630 635 640

Arg His Ile Leu Arg Arg Leu Asn Pro Glu Gly Lys Pro Leu Pro Ile
645 650 655

Leu Arg Ile Gly Glu Gly Ile Glu Asn Leu Val Arg Glu Ser Ile Arg
660 665 670

Gln Thr Ala Met Gly Thr Tyr Thr Ala Leu Ser Ser Arg His Lys Thr
675 680 685

Gln Ile Leu Gln Leu Ile Glu Gln Ala Leu Lys Gln Ser Ala Lys Leu
690 695 700

Phe Ile Val Thr Ser Val Asp Thr Arg Arg Phe Leu Arg Lys Ile Thr
705 710 715 720

Glu Ala Thr Leu Phe Asp Val Pro Ile Leu Ser Trp Gln Glu Leu Gly
725 730 735

Glu Glu Ser Leu Ile Gln Val Val Glu Ser Ile Asp Leu Ser Glu Glu
740 745 750

Glu Leu Ala Asp Asn Glu Glu
755

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Ile Asp Ala Thr Ser Glu Ala Glu Ile Ser Ala Pro Arg Trp Leu Leu
1 5 10 15

Ser Met Gly Pro Asn Ser Gly Cys Gln Arg Asn Val Val Lys Cys Val
20 25 30

Val Ala Trp Gly Ile Tyr Gly Arg Val Val Leu Tyr Lys Ala Trp Arg
 35 40 45

Arg Thr Cys
 50

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ser Arg Gly Asp
 1

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Trp Gln Gln Ser Phe Ala Ile Ser Phe Tyr Glu Tyr Asn Arg Ala Ser
 1 5 10 15

Leu Arg Ala Ala Ser Asp Gly Leu Lys Arg Arg His Gln Val Pro Val
 20 25 30

Gly Glu Ala Leu Leu Gly Arg Val Ile Asp Gly Phe Gly Arg Pro Leu
 35 40 45

Asp Gly Arg Glu Leu Pro Asp Val Cys Trp Lys Asp Tyr Asp Ala Met
 50 55 60

Pro Pro Pro Ala Met Val Arg Gln Pro Ile Thr Gln Pro Leu Met Thr
 65 70 75 80

Gly Ile Arg Ala Ile Asp Ser Val Ala Thr Cys Gly Glu Gly Gln Arg
 85 90 95

Val Gly Ile Phe Ser Ala Pro Gly Val Gly Lys Ser Thr Leu Leu Ala
 100 105 110

Met Leu Cys Asn Ala Pro Asp Ala Asp Ser Asn Val Leu Val Leu Ile
 115 120 125

Gly Glu Arg Gly Arg Glu Val Arg Glu Phe Ile Asp Phe Thr Leu Ser
 130 135 140

Glu Glu Thr Arg Lys Arg Cys Val Ile Val Val Ala Thr Ser Asp Arg
 145 150 155 160
 Pro Ala Leu Glu Arg Val Arg Ala Leu Phe Val Ala Thr Thr Ile Ala
 165 170 175
 Glu Phe Phe Arg Asp Asn Gly Lys Arg Val Val Leu Leu Ala Asp Ser
 180 185 190
 Leu Thr Arg Tyr Ala Arg Ala Ala Arg Lys Ser Leu Trp Arg Arg Arg
 195 200 205
 Asp Arg Gly Phe Trp Arg Ile Ser Pro Gly Val Phe Ser Ala Leu Pro
 210 215 220
 Arg Leu Leu Glu Arg Thr Gly Met Gly Glu Lys Gly Ser Ile Thr Ala
 225 230 235 240
 Phe Tyr Thr Val Leu Val Glu Gly Asp Asp Met Asn Glu Ala Val Gly
 245 250 255

Gly

- (2) INFORMATION FOR SEQ ID NO:93:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Ser Pro Phe Thr Ala
 1 5

- (2) INFORMATION FOR SEQ ID NO:94:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Trp Thr Tyr Cys Thr Ile Pro Thr Ala Cys Arg Glu Gly Ala Leu Ser
 1 5 10 15

Cys His

- (2) INFORMATION FOR SEQ ID NO:95:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Arg Val Gly Asn Ala Gln Pro Arg Phe Ser Ser Arg Tyr Gln Pro
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ala Ser Ser Thr Gly Gly Asp Ile Ala Thr Val Pro Gly Ala Leu Pro
 1 5 10 15

Gly Gly

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Thr Val Asn Thr His Trp Gly Ile Pro Ala Arg Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Tyr Leu Ser Gly Tyr Leu His Ile Phe Ala Thr Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

Ser Met Arg Thr Arg Ala Thr Tyr Arg Lys Ile Thr Pro Asn Thr His
 1              5              10              15
Arg Val Ile Met Glu Thr Leu Leu Glu Ile Ile Ala Arg Leu Lys Ser
              20              25              30
Asn Tyr Ala Ala Ser Leu Pro Tyr Leu Ile Ser Ser Asn Arg Arg Leu
              35              40              45
Leu Arg Asn Ser Arg Phe Ala Arg Arg Ala Leu
              50              55

```

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Gln Cys Leu Pro Asp
 1              5

```

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

Trp Ala Gly Lys Val Arg Tyr Leu Val Ile Tyr Cys Trp Ile Arg Asn
 1              5              10              15
Asn Lys Trp Pro Gly Tyr Ser Leu Arg Arg Arg Ala Phe
              20              25

```

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Arg Asn Gly Lys Gln Leu Glu Asn Gln Tyr Gln Gln Leu Val Ser Arg
1 5 10 15

Arg Ser Glu Leu Gln Lys Asn Phe Asn Ala Leu Met Lys Lys Lys Glu
20 25 30

Lys Ile Thr Met Val Leu Ser Asp Ala Tyr Tyr Gln Ser
35 40 45

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Gly Lys Ser Trp Val Ala Met Pro Val Leu Ser Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Arg Gly Gly Gly Gly Thr Tyr Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Thr Thr His Ala Pro Gly Ile Thr His Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Ser Ser Cys Ser Ile Glu
1 5

Glu Arg Gly Phe His Ala Thr Leu Ser Cys
1 5 10

Trp Arg Leu Ser
1

Arg Cys Arg Val
1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

(2) INFORMATION FOR SEQ ID NO:111:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ala Ala Tyr Gly Val Tyr Asn Phe Pro Gly Asp Ile Leu Cys
20 25 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Pro Leu Val Ser
20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Val Cys Asn Asn Ile Gln Tyr Ser Lys Gly His Tyr Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Ile Ile Ile Met Ser Trp Val Gly Cys Gly Leu Gln Asn Asn Ala Gly
1 5 10 15

Ser Ala Gly Val Lys Gly
20

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Leu Ala Pro Leu Ile Asp Arg Leu Ser Ile Leu Asn Cys Tyr Met Glu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Asn Gly Gly Trp Arg Arg Tyr Cys Lys Pro Val Met Gln Pro Ser
1 5 10 15

Val Arg Thr Ser Arg Gln His Pro Ala Val Ile Tyr His Ile Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Arg Cys Ile Leu Asn Gly Gln Leu Lys Ser Met Ser Ser Ile Ala Leu
1 5 10 15

Phe Leu His Gly Gln Arg Val Phe Cys Ala Ile
20 25

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Ser Glu Ser Phe Leu Leu Ser Asp Asn Arg Phe Ile Leu Pro Leu Leu
1 5 10 15

Trp

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Ser Leu Tyr Ile Gln Ala Gly Ala Ser Leu His
1 5 10

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ser Asn Leu Ser Leu Ser Lys Ser Ala Trp Ala Phe Gly Phe Ile Ala
1 5 10 15

Ser Ala Thr Ser Asp Ser Val Phe Leu Leu Phe Asn Tyr Leu Gly Glu

Ser Thr Gln Gly Cys Cys
35

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gln Arg Ile Thr Arg
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Asn Leu Thr Asn
1

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ser Arg Ile Ser Lys Arg Tyr Leu Arg Gln Gly Ala Gln Cys Gln Arg
1 5 10 15

Val Thr Glu Arg Leu Gln Ser Asn Leu Ser Arg Tyr His Asn Arg Cys
20 25 30

Ser Leu Arg Ser Asp Val Arg Val Trp Lys Leu Asp Asn Tyr Asp Asn
35 40 45

Leu Lys Arg Gly Thr Phe Cys Leu
50 55

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Val Asp Val Leu Arg Gln Arg
 1 5

- (2) INFORMATION FOR SEQ ID NO:125:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Thr Val Leu Leu Gly Lys Val Ser
 1 5

- (2) INFORMATION FOR SEQ ID NO:126:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Leu Pro Val Ala Met Asn Leu Trp Cys Val Leu His Val Gly Ile Phe
 1 5 10 15

Ala Lys Ile Gln Arg Lys Pro Asp Lys Lys Asn Asn Met Arg Thr Ile
 20 25 30

- (2) INFORMATION FOR SEQ ID NO:127:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Arg Ser Arg Ser Cys His Glu Arg Tyr Ser Met Ser Leu Pro Asp Ser
 1 5 10 15

Pro Leu Gln Leu Ile Gly Ile Leu Phe Leu Leu Ser Ile Leu Pro Leu
20 25 30

Ile Ile Val Met Gly Thr Ser Phe Leu Lys Leu Ala Val Val Phe Ser
35 40 45

Ile Leu Arg Asn Ala Leu Gly Ile Gln Gln Val Pro Pro Asn Ile Ala
50 55 60

Leu Tyr Gly Leu Ala Leu Val Leu Ser Leu Phe Ile Met Gly Pro Thr
65 70 75 80

Leu Leu Ala Val Lys Glu Arg Trp His Pro Val Gln Val Ala Gly Ala
85 90 95

Pro Phe Trp Thr Ser Glu Trp Asp Ser Lys Ala Leu Ala Pro Tyr Arg
100 105 110

Gln Phe Leu Gln Lys Asn Ser Glu Glu Lys Glu Ala Asn Tyr Phe Arg
115 120 125

Asn Leu Ile Lys Arg Thr Trp Pro Glu Asp Ile Lys Arg Lys Ile Lys
130 135 140

Pro Asp Ser Leu Leu Ile Leu Ile Pro Ala Phe Thr Val Ser Gln Leu
145 150 155 160

Thr Gln Ala Phe Arg Ile Gly Leu Leu Ile Tyr Leu Pro Phe Leu Ala
165 170 175

Ile Asp Leu Leu Ile Ser Asn Ile Leu Leu Ala Met Gly Met Met Met
180 185 190

Val Ser Pro Met Thr Ile Ser Leu Pro Phe Lys Leu Leu Ile Phe Leu
195 200 205

Leu Ala Gly Gly Trp Asp Leu Thr Leu Ala Gln Leu Val Gln Ser Phe
210 215 220

Ser
225

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met Ile Leu Asn

1

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Arg Asn Phe Tyr Gly Ser Ser Phe Leu Arg Leu Cys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Cys Trp Trp His Arg
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Leu Val Ser Ser
1

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Ala Leu Phe Arg Pro
1 5

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Leu Lys Tyr Arg Thr Lys Arg Tyr Ser Ser
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:134:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Leu Asn Tyr Trp Gln Leu Gln
 1 5

- (2) INFORMATION FOR SEQ ID NO:135:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Trp Ser Ala Thr His Gly Leu Ala Val Ser Cys
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:136:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ile Ile Pro Gly Arg
 1 5

- (2) INFORMATION FOR SEQ ID NO:137:
 - (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Cys Tyr Glu Leu Glu Ser Met Val Glu Trp His Asn Arg
1 5 10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Met Ser Gly Leu Leu His Trp Leu Trp Leu Leu Phe Asp His
1 5 10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Ala Phe Leu Tyr Tyr Phe Pro Tyr
1 5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Lys Val Ala Val
1

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Gly Pro His Phe Tyr Val Met Ala Cys Leu Cys His Leu Pro Phe Arg
 1 5 10 15
 Tyr Tyr Gln Ser Phe Thr Ser Arg Arg Leu
 20 25

- (2) INFORMATION FOR SEQ ID NO:142:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Cys Ile Leu Val Lys Ile Thr Val Gly
 1 5

- (2) INFORMATION FOR SEQ ID NO:143:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Ser Leu Glu Arg
 1

- (2) INFORMATION FOR SEQ ID NO:144:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Leu Leu Val Phe Gln Leu Gly Phe Val Arg Arg Phe Pro Phe Gly Pro
 1 5 10 15
 Leu Ile Trp Arg Gly Phe Cys Leu Ile Leu Tyr Val Ala Arg Gln Trp
 61

009111"2094760

Val Arg Tyr Ser Ile Leu Gln
35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Lys Leu Lys Pro His Phe Leu Ala Cys Phe Ser Ala Ser Ser Cys Val
1 5 10 15

Leu Phe Ser Leu
20

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Ala Ala Ala Trp Ser Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Thr Phe Cys Met Ser His Ile Asn Ile Tyr His Gln Gly Val Leu Tyr
1 5 10 15

Tyr Leu Thr Ser Asn Phe
20

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Asn Ile Ser Arg Gln Ser Gly Glu Arg Phe Ile Asn Tyr Val Ser Ala
 1 5 10 15
 Ser Leu Phe Leu Pro
 20

- (2) INFORMATION FOR SEQ ID NO:149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Tyr Val Trp Tyr
 1

- (2) INFORMATION FOR SEQ ID NO:150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Pro Ile Trp Leu
 1

- (2) INFORMATION FOR SEQ ID NO:151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Ile Gly Arg His Asn Asn
 1 5

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Cys Phe Ser Ser Gln Cys Arg Ser Lys Val Tyr Trp Phe Tyr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:153:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Xaa Pro Asp Leu Ile Pro Leu Cys Ser Ser Ser Leu Phe Gly
 1 5 10

(2) INFORMATION FOR SEQ ID NO:154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Ile Leu Tyr Leu Ser Lys Arg Leu Val Ser Ile Cys Met Ser Glu Lys
 1 5 10 15

Thr Glu Gln Pro Thr Glu Lys Lys Leu Arg Asp Gly Arg Lys Glu Gly
 20 25 30

Gln Val Val Lys Ser Ile Glu Ile Thr Ser Leu Phe Gln Leu Ile Ala
 35 40 45

Leu Tyr Leu Tyr Phe His Phe Phe Thr Glu Lys Met Ile Leu Ile Leu
 50 55 60

Ile Glu Ser Ile Thr Phe Thr Leu Gln Leu Val Asn Lys Pro Phe Ser
 65 70 75 80

Tyr Ala Leu Thr Gln Leu Ser His Ala Leu Ile Glu Ser Leu Thr Ser
 85 90 95

Ala Leu Leu Phe Leu Gly Ala Gly Val Ile Val Ala Thr Val Gly Ser
 100 105 110

Val Phe Leu Gln Val Gly Val Val Ile Ala Ser Lys Ala Ile Gly Phe
 115 120 125

Lys Ser Glu His Ile Asn Pro Val Ser Asn Phe Lys Gln Ile Phe Ser
 130 135 140

Leu His Ser Val Val Glu Leu Cys Lys Ser Ser Leu Lys Val Ile Met
 145 150 155 160

Leu Ser Leu Ile Phe Ala Phe Phe Phe Tyr Tyr Tyr Ala Ser Thr Phe
 165 170 175

Arg Ala Leu Pro Tyr Cys Gly Leu Ala Cys Gly Val Leu Val Val Ser
 180 185 190

Ser Leu Ile Lys Trp Leu Trp Val Gly Val Met Val Phe Tyr Ile Val
 195 200 205

Val Gly Ile Leu Asp Tyr Ser Phe Gln Tyr Tyr Lys Ile Arg Lys Ala
 210 215 220

Ile
 225

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Val Lys Met Thr

1

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Asn Arg Ser Ile Lys Ile Trp Arg Ala Thr Leu Lys

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(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Arg Arg Gly Val Gly Asn Ala Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:158:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Asn Thr Lys Trp Glu Phe Ser Ser Ile Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:159:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Thr Ile Cys Cys Gly Ser Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:160:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Ser Asn Ala Tyr Cys Gly Leu Ser Trp Leu Ser Ser His Arg Tyr Ala
 1 5 10 15

Asn Thr Thr Arg Pro Gly Lys Arg Gln
 20 25

(2) INFORMATION FOR SEQ ID NO:161:
 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Thr Gln Leu His Pro Arg Cys
 1 5

(2) INFORMATION FOR SEQ ID NO:162:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Ala Gly Pro Leu Ile Ile Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:163:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Ser Gly Thr Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Thr Arg Cys Ser Leu Val Thr Tyr Gly Asp Glu Asp Arg Leu Cys Ala
 1 5 10 15

Phe Tyr Arg Asn Thr Ile Asn Ala Phe Gly Met Leu Leu Gln Ala Thr
 20 25 30

Ala Lys Val Lys Arg Val Ile Ala Tyr Arg Ala Val Leu Asp Asp Lys
 35 40 45

Gly Glu Arg Leu Lys Ile Ile Ala Phe Ser Leu Ala Gln Ala Pro Asp
 50 55 60

Ser Val Leu
 65

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Trp Ile Gly Ala Ser Glu Trp Thr Arg Thr Thr Arg Pro Pro Pro Cys
 1 5 10 15

Gln Gly Gly Ala Leu Thr Asn
 20

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Ala Met Asn Gly Asn Val Val Gly Asp Asn Gly Asp Glu Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Arg His Asn Arg Asn Glu Ala Arg Gly Lys Ser Gln Phe Ser Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids

68

09714602 111600

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Asn His Leu Ile Ala Val Glu Ile Cys Asn Met Ser Arg Lys
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:169:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Pro Pro Cys Asp Gly Tyr Arg Arg Ile Ile Gly Ala Arg Cys Lys Met
 1 5 10 15

Met Ala Asp Gly
 20

- (2) INFORMATION FOR SEQ ID NO:170:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Arg Ile Arg Ser Ile Ile Asn Thr Ala Ala Glu Val Arg Pro Met Met
 1 5 10 15

Asn Pro Ile Gln Lys Pro Ala Gly Pro Ile Arg Ser Thr Thr Lys Ser
 20 25 30

Val Asn Ala Arg Ile
 35

- (2) INFORMATION FOR SEQ ID NO:171:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Pro Leu Gly Lys Pro Asn Thr Gln
1 5

(2) INFORMATION FOR SEQ ID NO:172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Ala Val Lys Val Ile Lys Lys Met Glu Arg Val Ser Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Pro Arg Arg Ile Pro Leu Pro Ile Thr Cys Ile Glu Ser Glu Ile Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Thr Ala Ala Ser Ser Ile Asn Cys Gly Lys Arg His Asp Leu Arg Val
1 5 10 15

Val Ile Val Glu Gln Ser Asn Met Leu Thr Gln Ser Asn Gly Lys Asn
20 25 30

Ser Gly Asn His Ser His Thr Asn Ala Asp Ala
35 40

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Thr Gly Thr Arg Cys Val Cys Ala Ser Ser Val Glu Pro Trp Pro Arg
 1 5 10 15
 Pro Ile Thr His Ser Asn Arg Tyr Arg Arg Ser Gln Arg His Arg Gln
 20 25 30
 Tyr Glu His Gln Arg Ala Lys Val Lys Arg Asn Leu Met Thr Gly Asp
 35 40 45
 Ile His Asn Thr
 50

(2) INFORMATION FOR SEQ ID NO:176:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Trp Arg Asn Gln Gln Arg Asn Asp Arg Lys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:177:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Arg His Phe Lys Glu Gln Pro Ala Gln Ser Ala Thr Pro Val Glu Ser
 1 5 10 15
 Gly Ala Ser

(2) INFORMATION FOR SEQ ID NO:178:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Arg Arg Tyr Arg Val Cys Gln Ser Leu Phe His Tyr Glu Tyr His Ala
1 5 10 15
Leu Asn Ala Arg Val
20

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Cys Lys Lys Ala Trp Arg
1 5

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Thr Ser Pro Asn Arg Pro Pro Gln Ser Gln Arg Arg Ser Arg Tyr Arg
1 5 10 15

Arg Val Pro Ala Tyr Gln Asn Gly His Arg
20 25

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Lys Tyr Ser Ser Pro Glu Tyr Ser Pro Ala Gly Pro Lys Ile Pro Ser
1 5 10 15

Pro Tyr Pro Val Trp Phe Trp Pro Asp Leu Arg Thr Gly Phe Ala Leu
20 25 30

Pro Glu Arg Lys Gly Ile Leu Arg Pro Thr Ala Ala Arg Glu Asp Asn
 35 40 45

Pro Arg Leu Tyr Arg Pro Ala Pro Asp Gln Tyr Tyr Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Cys Ile Arg His Ser Thr Gly Arg Ser Ser Pro Ala Arg Arg Gln Ser
 1 5 10 15

Pro Pro Ala Arg Thr Leu Val Glu Pro Asp Ala Arg Tyr Ala His Asp
 20 25 30

Gly Arg Ser His
 35

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Val Ala Gln Ser Gln Ala Ser Arg Pro Ala Val Ser Arg Asp Gln Thr
 1 5 10 15

Lys Trp Arg Glu Ala Asp Arg Gly Ala Asp Ser Asp Gly Ser His Val
 20 25 30

Arg Ser Ala Ile Ala Ser Arg His Asp Gly Ile Asp Glu Ser Ile Ala
 35 40 45

Val Tyr Thr Thr Cys Ala Arg Ile Thr Gly Ile
 50 55

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Thr Leu Ile Thr Asp Ala Leu His Trp Tyr Thr Ser Ala Arg Ile His
1 5 10 15
Leu Leu Phe Cys Cys Tyr Met Lys Asp
20 25

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Lys Ala Ala Glu Val Ala Ala Lys Arg Asn Ser Arg Gly Asn Phe Ser
1 5 10 15
Leu Leu

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Gly Ile Thr Ile Ser Pro Val Lys Lys Gln Leu Leu Thr Ala His
1 5 10 15
Cys Trp Gln Ala Val Phe Pro Pro Ala Ile Val Leu Asn Ser Ser Ala
20 25 30
Phe Ile Tyr Phe Arg Ser
35

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Arg Tyr Val Tyr Gly Asp Arg Thr Gly Tyr Arg Glu Thr Gly Ile Asp
74

009111 2094160

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15

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Cys Arg Thr Glu Pro Gly Ala Asn

1

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(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Thr Ile Ala Glu Arg

1

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(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Ser Ile His Gln

1

(2) INFORMATION FOR SEQ ID NO:191:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

Arg Gln Cys Phe Ile Thr Ala Gly Tyr Val Asp Gln Thr Asn Gly Leu

1	5					10					15				
Tyr	Ala	Val	Asn	Gly	Arg	Arg	Arg	Leu	Ser	Cys	Gln	Asn	Ile	Thr	Ala
			20					25					30		
Gln	His	Ala	Lys	Arg	Leu	Ile	Ser	Trp	Ile	Thr	Trp	His	Glu	Gly	Ser
			35					40					45		
Ser	Tyr	Ser	Ile	Ser	Tyr	Cys	Pro	Tyr	Val	Leu	Ser	Tyr	Gly	Met	
			50					55					60		

(2) INFORMATION FOR SEQ ID NO:192:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

(2) INFORMATION FOR SEQ ID NO:193:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

(2) INFORMATION FOR SEQ ID NO:194:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Ser Ala Val Tyr
20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

(2) INFORMATION FOR SEQ ID NO:196:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

Phe Phe Lys Arg Thr Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:197:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Arg Asn Ala Glu Ser Asp Gly Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:198:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Leu Met Ala Lys Val Thr Ile Ala Leu Pro Thr Tyr Asp Glu Gly Ser
 1 5 10 15
 Asn Ala Ser Pro Ser Ser Val Ala Val Phe Ile Lys Tyr Ser Pro Gln
 20 25 30
 Val Asn Met Glu Ala Phe Arg Val Lys Ile Lys Asp Leu Ile Glu Met
 35 40 45
 Ser Ile Pro Gly Leu Gln Tyr Ser Lys Ile Ser Ile Leu Met Gln Pro
 50 55 60
 Ala Glu Phe Arg Met Val Ala Asp Val Pro Ala Arg Gln Thr Phe Trp
 65 70 75 80
 Ile Met Asp Val Ile Asn Ala Asn Lys Gly Lys Val Val Lys Trp Leu
 85 90 95
 Met Lys Tyr Pro Tyr Pro Leu Met Leu Ser Leu Thr Gly Leu Leu Leu
 100 105 110
 Gly Val Gly Ile Leu Ile Gly Tyr Phe Cys Leu Arg Arg Arg Phe
 115 120 125

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Ala Asp Leu Ile Pro Arg Cys Cys Asn Phe Ile Val Ile Ser Gly Asn
 1 5 10 15
 Leu Leu Val Thr Leu Tyr Arg Asn Gly Trp Ile Ser Trp Ala Phe Ile
 20 25 30
 Phe Lys Leu Leu Ala Leu Trp Arg Ser Ala Arg Val Gly Ser Ser Ser
 35 40 45

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Gln Ser Val Lys

1

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Thr Lys Arg Lys Leu Cys Tyr Ser Ser Leu Phe Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Ala Lys Thr Ala Gly Ser Ser Cys Ala Ala Tyr Ile Gly Ile Cys
1 5 10 15

Leu Trp Ala Gly Ile Ile Gln Thr Gln Val
20 25

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

Leu Phe Tyr Ala Thr Arg Val Ser Ala Ile Ala Ser Thr Val Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Asp Leu Ala Ala Ile Trp Leu Val Gly Ala Lys Arg Trp Gln Ile Thr
 1 5 10 15

Ser Ser Ala Ser Asp Ala Thr Asn Cys Ile Ala Asp Arg Tyr Arg His
 20 25 30

Ser

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Ser Gly Ser Ala
 1

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Arg Cys Gly Phe Tyr Met Arg Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Tyr Tyr Tyr Pro Leu Arg Ser Val Tyr Phe Gly Arg Arg Leu Leu Leu
 1 5 10 15

Pro Arg Leu Ser Ser Trp Ser Ile Cys Tyr Glu Phe Tyr Phe Thr Ser
 20 25 30

Ser Asp Gly Asn
 35

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Ala Thr Arg Ser Lys Tyr Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Val Thr Val Asp Asn Ile Thr Ile Asn Phe Ile Cys Ala Arg Ala Thr
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Glu Ser Phe Thr Cys Tyr Cys Glu Leu Arg Leu Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Lys Asn His Pro Arg Arg Leu Ser Leu Ser Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Ala Ala Thr Arg Thr Ser Val Leu Ala

1 5

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Lys Tyr Ala Gly Lys Asn Gly Ser Gly Met Ala Gly Thr Ala Cys Lys

1 5 10 15

Thr Phe Thr Arg Arg

20

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Lys Ser Ile Ser Phe Ile Gly Arg Ser Arg Ser Ala Ser Tyr

1 5 10

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

Tyr Arg Thr Gly Ser Val Gly Leu Val Arg Pro Thr Val Gly Arg Gln
 1 5 10 15
 Cys Tyr Val Pro Ser Ser Gly Thr Pro Gly His Gly Tyr Gly Gly Arg
 20 25 30
 Gly Ser Ala Leu Phe Ala Tyr Ser Ser
 35 40

(2) INFORMATION FOR SEQ ID NO:216:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

Lys Arg Gly Ile Asp Ala Arg Asn Phe Trp Gln Ala Val Tyr Val Asp
 1 5 10 15
 Tyr Arg Ala Trp Phe Leu Ser Arg Ser Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Thr Phe Leu Asn Thr Ile Cys Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Ile Phe Thr Phe Ser Ser Phe Gln Arg Val Thr Glu Met Val Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Ile Leu Lys Leu Met Arg
1 5

(2) INFORMATION FOR SEQ ID NO:220:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Arg Pro Leu Gln His Leu Pro Leu Ala Arg Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:221:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

Arg Asn Lys Arg Leu Phe Arg Leu Gln Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:222:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein.
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

Leu Ser Arg Ser Tyr Arg Lys Arg Arg Gly Gln Arg Ser Met Arg Arg
1 5 10 15

Trp Lys Lys

(2) INFORMATION FOR SEQ ID NO:223:
(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Val Val Asn Cys Ala Lys Ile Ile Asn Ser Leu Met Leu Arg Asn Trp
 1 5 10 15

Ser Ala Asp Ser Arg Leu Cys Cys Val
 20 25

(2) INFORMATION FOR SEQ ID NO:224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Asn Lys Tyr Arg Arg Ile Met Gly Gln Arg Cys Val Arg Leu Pro Lys
 1 5 10 15

Arg Ile Val Ile Leu Ile Tyr Arg Met Arg Ile Lys Leu Ser Leu Leu
 20 25 30

Gln Trp Arg Leu Leu Pro Ala Gly Cys Gln Lys Arg Lys Asn Ala Ile
 35 40 45

Cys Asn Arg Asn Trp Ile Arg Tyr Ser Gly Gly Gly Met Gly Thr Cys
 50 55 60

Arg Phe
 65

(2) INFORMATION FOR SEQ ID NO:225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 178 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Phe Thr Gly Thr Trp Arg Ser Gly Tyr Arg Thr Leu Ser Ser Leu Lys
 1 5 10 15

Arg Phe Met Gln Gln Ala Ile Asp Asn Asp Glu Met Pro Leu Ser Gln
 20 25 30

Trp Phe Arg Arg Val Ala Asp Trp Pro Asp Arg Cys Glu Arg Val Arg
 35 40 45

Ile Leu Leu Arg Ala Val Ala Phe Glu Leu Ser Ile Cys Ile Glu Pro
 50 55 60

Ser Glu Gln Ser Arg Leu Ala Ala Ala Leu Val Arg Leu Arg Arg Leu
 65 70 75 80

Leu Leu Phe Leu Gly Leu Glu Lys Glu Cys Gln Arg Glu Glu Trp Ile
 85 90 95

Cys Gln Leu Pro Pro Asn Thr Leu Leu Pro Leu Leu Leu Asp Ile Ile
 100 105 110

Cys Glu Arg Trp Leu Phe Ser Asp Trp Leu Leu Asp Arg Leu Thr Ala
 115 120 125

Ile Val Ser Ser Ser Lys Met Phe Asn Arg Leu Leu Gln Gln Leu Asp
 130 135 140

Ala Gln Phe Met Leu Ile Pro Asp Asn Cys Phe Asn Asp Glu Asp Gln
 145 150 155 160

Arg Glu Gln Ile Leu Glu Thr Leu Arg Glu Val Lys Ile Asn Gln Val
 165 170 175

Leu Phe

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Tyr Leu Ala Phe Asn Ile
 1 5

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Val Asn Trp Leu Ser Gly Ser Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:228:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

Gly Val Arg Met Asp Trp Asp Leu Ile Thr Glu Arg Asn Ile Gln Leu
1 5 10 15
Phe Ile Gln Leu Ala Gly Leu Ala Glu Arg Pro Leu Ala Thr Asn Met
20 25 30
Phe Trp Arg Gln Gly Gln Tyr Glu Thr Ile Ile Thr Val Val Phe Ser
35 40 45
Tyr Val Arg Tyr Ser Ser Lys Pro Ser
50 55

(2) INFORMATION FOR SEQ ID NO:229:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

Thr Lys Asn Cys Phe Leu Lys Arg Trp Leu Thr Gly Asn Pro Gln Arg
1 5 10 15
Ser Arg Val Phe Leu Asn Asp Tyr Phe Cys Cys Ala Met Gly Leu Gln
20 25 30

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Val Val Leu His Leu Phe Pro Ala Pro Pro Ser Ser Gly Tyr Asp Tyr
1 5 10 15
Ile Ile Asp Lys
20

(2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Asn Phe Xaa Glu Ser Gln Cys Val His Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:232:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Val Arg Glu Ser Gly Arg Asn Ser Gly Ser Val Tyr Ala Arg Val Gly
1 5 10 15

Arg Ile Trp Phe Trp Arg Arg Cys Tyr
20 25

(2) INFORMATION FOR SEQ ID NO:233:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Cys Cys Tyr Pro Cys Arg Pro Gly Trp Leu Ile Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:234:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Leu Leu Ser Thr Leu Cys Phe Gln
1 5

(2) INFORMATION FOR SEQ ID NO:235:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Leu Leu Phe Ile Leu Val Thr Leu Ser Ile Tyr Arg Tyr Phe Arg Leu
1 5 10 15

Tyr Tyr Leu Leu Leu His Tyr Ile Val Cys His Ser Gln Ser Ala His
20 25 30

His Gly Trp Tyr Cys Tyr Asn Ile Met Pro Val Ile Leu Trp Met Leu
35 40 45

Ser Val Ser Leu Ser
50

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Glu Glu Ile Ser Pro Leu Gly Trp Ser Tyr Leu Pro Ser Leu Leu Ser
1 5 10 15

Cys Asn Leu Leu Ser Leu Gln Lys Val Ser Arg Gly Trp Arg Lys Leu
20 25 30

Ala His Val Ser Arg Leu Met Gly Cys Gln Ala Asn Lys
35 40 45

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Val Ser Met Ala Ile Cys Val Pro Glu Leu Ser Met Gln Thr Met Pro
 1 5 10 15

Val His

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Asp Ser Met Ser Ser Arg Lys Ala Ala Phe Ser Val Arg Trp Thr Val
 1 5 10 15

Arg

(2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

Asn Leu Leu Lys Ala Ile Arg Leu Pro Val Leu Leu Leu Phe Trp
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:240:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Thr Leu Ser Ala Val Ser Leu Ser Leu Ser Tyr Asn Met Ile Cys Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Val Arg Leu Phe Thr Leu Ile Ala Tyr Cys Gln Ser Glu Met Val Tyr
1 5 10 15

Val Gly Lys Phe His Arg Cys
20

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Phe Pro Leu Ala Arg Glu Leu Leu Ser Pro Val Ser Arg Val Arg Asn
1 5 10 15

Ala Arg Thr Trp Arg Gln Ser
20

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Val Leu Lys Leu Pro Asp Asn Leu Ser Arg Ser Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Pro Leu Trp Phe
1

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Cys Ser Ser Leu

1

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Phe Leu Ala Phe Leu Leu Ser Leu Ser Leu Ser Phe Gln Arg Cys
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

His Cys Gln Leu Ser Ser Phe Ala Ala Lys Ser Leu Trp Phe Pro Gln
 1 5 10 15

Met Ala Ser Lys His Arg Lys Lys Ile Val Trp Phe Pro Ala His Val
 20 25 30

Leu

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Ser Tyr Val Leu Ala Arg Arg Tyr Ile Leu Pro Thr
 1 5 10 92

00911"20941260

(2) INFORMATION FOR SEQ ID NO:249:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Phe Val Ile Leu Thr Pro
1 5

(2) INFORMATION FOR SEQ ID NO:250:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Asp Gly Phe Tyr Leu Arg Ile Pro Ala Ser Leu Ser Leu Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:251:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

Ile Leu Arg Phe Cys Leu Asn Pro Pro Lys Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:252:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Arg Tyr Cys Tyr Ile Arg Asn Pro Tyr Leu Val Tyr Leu Phe Pro Leu
1 5 10 15

Arg Arg Ile Ile Tyr
20

(2) INFORMATION FOR SEQ ID NO:253:

Ala Arg Thr Leu Val Trp Trp Val Thr Ala Arg Arg Tyr Arg Thr Gly
1 5 10 15

Asn Val Ser Cys Phe Gly Ile Trp Glu Ser Leu Leu Val Phe Arg Lys
1 5 10 15

Met Arg Trp Lys Lys Thr Thr Leu Ser Trp
1 5 10

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Lys Ser Phe Ser Ala Ser Tyr Pro Leu Ile Lys Ser Leu Lys Leu Cys
 1 5 10 15
 Asn Gly Leu Tyr Gln Ser Gly Phe Leu Leu Glu Ile Tyr Val Leu Phe
 20 25 30
 Ser Ala Pro
 35

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu Thr Gly Arg His Val Lys Lys Met Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Gln Asn Met Ser Val Ser Arg Phe Val Val Ile Phe Cys Val Val Leu
 1 5 10 15
 Ile Arg Lys Glu Asn Arg Cys Arg Phe Cys Gly Ser Ala Lys Val Leu
 20 25 30
 Lys Thr Ser Cys Val Asn Pro Phe Ala Arg Arg Gln Trp Gly Pro Ile
 35 40 45
 Leu Arg Cys Arg Leu Val Ile Arg Arg Arg Ser Cys Asn Leu Ser Ser
 50 55 60
 Arg Arg
 65

(2) INFORMATION FOR SEQ ID NO:259:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Ser Ser Gln Pro Asn Tyr Ser Leu Ser Leu Leu Ser Thr Pro Asp Val
 1 5 10 15
 Ser Cys Glu Lys Leu Gln Lys Pro Pro Cys Ser Thr Tyr Arg Phe Cys
 20 25 30
 His Gly Arg Asn
 35

- (2) INFORMATION FOR SEQ ID NO:260:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 8 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Glu Arg Arg Ala Leu Tyr Lys Trp
 1 5

- (2) INFORMATION FOR SEQ ID NO:261:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Lys Val Leu Thr Leu Ala Lys Arg Ser Trp Arg Thr Met Lys Asn Glu
 1 5 10 15
 Leu Met Gln Arg Leu Arg Leu Lys Tyr Pro Pro Pro Asp Gly Tyr Cys
 20 25 30
 Arg Trp Gly Arg Ile Gln Asp Val Ser Ala Thr Leu Leu Asn Ala Trp
 35 40 45
 Leu Pro Gly Val Phe Met Gly Glu Leu Cys Cys Ile Lys Pro Gly Glu
 50 55 60
 Glu Leu Ala Glu Val Val Gly Ile Asn Gly Ser Lys Ala Leu Leu Ser
 96

65 70 75 80

Pro Phe Thr Ser Thr Ile Gly Leu His Cys Gly Gln Gln Val Met Ala

 85 90 95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Leu Val Asn Val Asp Glu Lys Ser Ala Asn Ser Ser Ile Leu His Cys
1 5 10 15
Leu Lys Arg Pro Glu Asn Val Val Ser Leu Leu Ser Gln Pro Leu Thr
20 25 30
Asp Pro Pro
35

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Gly Arg Cys Leu Trp Pro Pro Arg
1 5

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Gln Asn Phe Phe Ala Ile Met Glu Ser Glu Ser Ser Cys Leu Pro Thr
1 5 10 15

His

(2) INFORMATION FOR SEQ ID NO:267:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Arg Val Met Pro Gly Pro His Gly Asn Arg Ser Gly Ala Gly Glu Thr
1 5 10 15
Ala Val Ser Gly Glu Tyr Arg Gln Ala Tyr Leu Val His Cys His Asp
20 25 30

(A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

Ser Trp Lys Leu Cys Trp Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:271:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Lys Ala Ile Thr Arg Gln Ala Tyr Arg Thr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:272:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Ser Ala Ala Thr Gly Asp Tyr Tyr Gly Thr Ala Asp Leu Pro Asp Ala
 1 5 10 15

Arg Phe Ser Ser Val Tyr Gln Thr Glu Arg Ile Asn Gly Leu Ala Arg
 20 25 30

Tyr Val Ile Leu Ser Phe Ile Val Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:273:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Glu Thr Thr Asn Gly Arg Val Ile His Ser Gly Ala Glu Leu Phe Asp
 1 5 10 15

Ala Thr Ala Ser Ser
 20

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Arg Ile Ser Ile Ser Ser Leu Ser Pro Gly Glu Ala Asn Tyr Arg Arg
 1 5 10 15

Ile Leu Met Arg Leu
 20

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Lys Arg Lys Lys Lys Leu Leu Trp Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

Ala Met Arg Ile Thr Lys Val Glu Gly Ser Leu Gly Leu Pro Cys Gln
 1 5 10 15

Ser Tyr Gln Asp Asp Asn Glu Ala Glu Ala Glu Arg Met Asp Phe Glu
 20 25 30

Gln Leu Met His Gln Ala Leu Pro Ile Gly Glu Asn Asn Pro Pro Ala
 35 40 45

Ala Leu Asn Lys Asn Val Val Phe Thr Gln Arg Tyr Arg Val Ser Gly
50 55 60

Gly Tyr Leu Asp Gly Val Glu Cys Glu Val Cys Glu Ser Gly Gly Leu
65 70 75 80

Ile Gln Leu Arg Ile Asn Val Pro His His Glu Ile Tyr Arg Ser Met
85 90 95

Lys Ala Leu Lys Gln Trp Leu Glu Ser Gln Leu Leu His Met Gly Tyr
100 105 110

Ile Ile Ser Leu Glu Ile Phe Tyr Val Lys Asn Ser Glu
115 120 125

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Arg Ala Ser Val Gly Gly Asp Thr Ser Asn Ala Arg Arg Tyr His Trp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Ala Asp Ile Glu Tyr Ala Thr Ile Ser Ser Thr Ala Arg Asp Ile Ile
1 5 10 15

Tyr His Lys Leu Ser
20

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Gly Val Asp Cys Arg Thr Met Leu Ala Ala Leu Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:280:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Arg Ala Asn Trp His Arg
1 5

(2) INFORMATION FOR SEQ ID NO:281:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Ser Ile Gly Tyr Arg Ser
1 5

(2) INFORMATION FOR SEQ ID NO:282:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

Ile Ala Ile Trp Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:283:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Met Gly Ala Gly Ala Val Ile Ala Ser Gln

1 5 10

(2) INFORMATION FOR SEQ ID NO:284:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Cys Asn Pro Leu Ser Glu Arg Ala Ala Asn Ile Leu Gln
1 5 10

(2) INFORMATION FOR SEQ ID NO:285:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Ser Thr Thr Ser Ala Ser Val Ala Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:286:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

His Tyr Phe Tyr Met Ala Asn Gly Phe Phe Ala Gln Tyr Ser Arg Arg
1 5 10 15

Ala Phe Cys

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

Ala Thr Thr Asp Leu Ser Cys Pro Ser Cys Gly Ser Pro Cys Ile Phe
 1 5 10 15

Arg Leu Val Pro Ala Tyr Ile Asn Arg Thr
 20 25

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

Val Tyr Arg Asn Arg His Gly Arg Ser Asp Ser Leu Leu Arg Arg His
 1 5 10 15

Gln Thr Arg Phe Phe Cys Tyr Ser Thr Thr Trp Gly Asn Leu Arg Lys
 20 25 30

Gly Val Ala Asp Arg Gly
 35

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

His Asp Glu Ile
 1

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

Arg Ile Ser Pro Gly Tyr Arg Asn Ala Thr Cys Val Arg Glu Pro Asn
 1 5 10 15

Val Lys Glu

(2) INFORMATION FOR SEQ ID NO:291:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Arg Asn Val Phe Ser Arg Thr
 1 5

- (2) INFORMATION FOR SEQ ID NO:292:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Ala Asp Thr Thr Thr Gly Ala Leu
 1 5

- (2) INFORMATION FOR SEQ ID NO:293:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

Gly Arg Thr Cys Glu Ser Gly Asn Trp Thr Ile Thr Thr Thr
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:294:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (iii) HYPOTHETICAL: NO
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Asn Gly Gly Arg Phe Ala Cys Arg Trp Met Phe Cys Ala Arg Gly Asp
 1 5 10 15

Asp Lys Ser Lys
 20

(2) INFORMATION FOR SEQ ID NO:295:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Pro Tyr Tyr Trp Ala Arg

1 5

(2) INFORMATION FOR SEQ ID NO:296:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Val Asp Cys Leu Trp Gln

1 5

(2) INFORMATION FOR SEQ ID NO:297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Ile Tyr Gly Ala Tyr Tyr Thr Leu Val Ser Leu Gln Lys Tyr Ser Val

1 5 10 15

Asn Leu Ile Arg Lys Ile Ile Cys Glu Gln Tyr Asn Ser Val Pro Gly

20 25 30

Arg Val Met Arg Asp Thr Val Cys Leu Tyr Pro Ile Arg Leu Cys Asn

35 40 45

(2) INFORMATION FOR SEQ ID NO:298:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Leu Val Tyr Cys Phe Cys Phe Gln Tyr Cys Leu Ser Leu Ser Ser Trp
1 5 10 15
Glu Leu Leu Ser Leu Asn Trp Arg Trp Tyr Phe Arg Phe Tyr Glu Met
20 25 30
Leu Trp Val Phe Asn Lys Ser Pro Gln Ile Ser His Cys Met Ala Leu
35 40 45
Arg Leu Tyr Phe Pro Tyr Ser Leu Trp Gly Arg Arg Tyr
50 55 60

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

Lys Ser Ala Gly Ile Arg Phe Arg Ser Leu Ala Leu Leu Ser Gly Arg
1 5 10 15
Leu Ser Gly Thr Val Lys His
20

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Arg Leu Ile Asp Ser Phe Cys Lys Lys Thr Leu Lys Arg Arg Lys Pro
1 5 10 15
Ile Ile Phe Gly Ile
20

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Asn Glu Pro Gly Leu Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:302:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Asn Leu Ile Leu Cys Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:303:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Phe Arg His Leu Arg
1 5

(2) INFORMATION FOR SEQ ID NO:304:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Arg Arg His Phe Gly Leu Asp Tyr Leu Phe Ile Phe Pro Phe Trp Leu
1 5 10 15

Leu Thr Cys Leu Phe Gln Ile Tyr Cys Trp Leu Trp Gly
20 25

(2) INFORMATION FOR SEQ ID NO:305:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Trp Cys Arg Arg

1

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Pro Phe His Tyr Arg Leu Ser Cys

1

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(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Tyr Phe Tyr Trp Gln Ala Val Gly Ile

1

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(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

His Trp Arg Asn Trp Tyr Arg Ala Phe His Glu

1

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(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Ile Asp Ala Ile Cys Asn Ala Thr Phe Met Asp Arg Pro Phe Tyr Val
1 5 10 15

Tyr Ala Gly Ser Val Gly Gly Ile Gly Ser Trp Cys His Arg Lys Pro
20 25 30

Cys Ser Gly Leu Asp Ser Asn Thr Gly Pro Asn Ala Thr Val His Asp
35 40 45

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Ile Ile Gly Asn Cys Asn Asn Leu Asn Gly Gln Leu Pro Met Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Arg Tyr Pro Val Glu Leu Tyr Pro Ala Asp Asn Val Thr Asn Trp Arg
1 5 10 15

Ala Trp Leu Asn Gly Thr Thr Gly Lys
20 25

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

Val Ala Tyr Cys Ile Gly Cys Gly Phe Tyr Ser Thr Ile Glu Pro Phe
1 5 10 15

Phe Ile Thr Ser Leu Ile Lys Lys Trp Gln Phe Arg Gly Arg Thr Phe
 20 25 30

Thr

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

Trp Arg Ala Tyr Val Thr Tyr Leu Ser Asp Ile Thr Asn His Leu Pro
 1 5 10 15

Ala Glu Asp Tyr Asp Ala Tyr Trp
 20

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Arg Leu Gln Leu Val Arg Val Ser His Trp Arg Gly Asp Tyr Trp Phe
 1 5 10 15

Phe Asn Trp Val Leu Cys Gly Gly Ser Leu Leu Gly Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Tyr Gly Gly Val Ser Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Tyr Phe Thr Trp Arg Asp Asn Gly Tyr Asp Ile Gln Phe Tyr Asn Arg
 1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Asn Leu Thr Phe Trp Leu Ala Phe Gln Pro Val Leu Val Cys Tyr Phe
 1 5 10 15

Leu Tyr Lys Arg Arg His Gly Val Tyr Ile Lys His Ser Val
 20 25 30

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

Val Ile Ser Ile Phe Thr Thr Arg Ala Tyr Phe Ile Ile
 1 5 10

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Pro Ala Ile Phe Lys Ile Tyr Pro Gly Arg Val Glu Asn Ala Leu Ser
 1 5 10 15

009477 2094760

Ile Met Tyr Gln Leu Leu Ser Ser Cys His Asn Met Tyr Gly Ile Ser
20 25 30
Arg Ser Gly Phe Arg Ser Phe Lys Ser Val Gly Thr Thr Ile Glu Cys
35 40 45
Val Phe Leu Leu Asn Ala Ala Gln Lys Tyr Ile Gly Ser Thr Asp Xaa
50 55 60
Leu Ile Ser Phe Pro Tyr Ala Leu His His Tyr Leu Val Glu Ser Asp
65 70 75 80
Lys Phe Tyr Ile Tyr Leu Lys Asp Trp Phe Pro Ser Val
85 90

(2) INFORMATION FOR SEQ ID NO:320:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Ala Arg Lys Gln Asn Ser Leu Gln Lys Arg Asn Tyr Val Met Ala Val
1 5 10 15
Arg Lys Gly Arg Leu Ser Lys Val Leu Lys
20 25

(2) INFORMATION FOR SEQ ID NO:321:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

His His Tyr Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:322:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

Leu Arg Phe Ile Cys Ile Phe Ile Ser Leu Leu Lys Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:323:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Leu Ser His Tyr Asn
1 5

(2) INFORMATION FOR SEQ ID NO:324:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Ile Asn His Phe Leu Met His
1 5

(2) INFORMATION FOR SEQ ID NO:325:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Leu Leu His Cys Cys Phe Trp Ala Leu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:326:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Leu Leu Leu Trp Val Ala Cys Phe Phe Arg Trp Gly Trp Leu Leu Pro
 1 5 10 15

Ala Arg Pro Leu Val Leu Lys Ala Ser Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Val Ile Leu Ser Arg Tyr Ser Leu Tyr Ile Ala
 1 5 10

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Asn Tyr Val Asn Pro Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Lys Leu Ser Cys Tyr Leu Leu Ser Leu Pro Phe Ser Phe Ile Ile Met
 1 5 10 15

Pro Val Leu Phe Gly Arg Tyr Arg Thr Val Gly
 20 25

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Pro Val Ala Cys Leu Trp Phe Leu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Asn Gly Tyr Gly
1

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Trp Phe Phe Ile Ser Ser Leu Ala Tyr Trp Thr Ile Leu Phe Asn Ile
1 5 10 15

Ile Arg Leu Glu Lys Leu Ser Lys Asn Glu
20 25

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

Arg Lys Thr Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

Arg	Ser	Gly	Gly	Arg	Pro	Ser	Asn	Glu	Asp	Ala	Ala	Ser	Glu	Met	Gln
1				5					10					15	
Ser	Glu	Ile	Gln	Ser	Gly	Ser	Leu	Ala	Gln	Ser	Val	Lys	Gln	Ser	Val
			20					25					30		
Ala	Val	Val	Arg	Asn	Pro	Thr	His	Ile	Ala	Val	Cys	Leu	Gly	Tyr	His
			35				40					45			
Pro	Thr	Asp	Met	Pro	Ile	Pro	Arg	Val	Leu	Glu	Lys	Gly	Ser	Asp	Ala
	50					55					60				
Gln	Ala	Asn	Tyr	Ile	Val	Asn	Ile	Ala	Glu	Arg	Asn	Cys	Ile	Pro	Val
65					70				75					80	
Val	Glu	Asn	Val	Glu	Leu	Ala	Arg	Ser	Leu	Phe	Phe	Glu	Val	Glu	Arg
				85					90					95	
Gly	Asp	Lys	Ile	Pro	Glu	Thr	Leu	Phe	Glu	Pro	Val	Ala	Ala	Leu	Leu
			100				105							110	
Arg	Met	Val	Met	Lys	Ile	Asp	Tyr	Ala	His	Ser	Thr	Glu	Thr	Pro	
		115				120						125			

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Met	Leu	Leu	Val	Cys	Phe	Phe	Arg	Pro	Leu	Arg	Arg	Leu	Arg	Gly
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

Arg	Ile	Glu	Gln	Cys	Leu	Thr	Ile	Lys	Val	Arg	Asp
											118

009714602-11600

1

5

10

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

Ser Leu Leu Ala Trp His Lys His Gln Ile Ala Tyr Tyr Lys Ile Lys
1 5 10 15

Gln Asp Asn Gly Leu Val Arg Leu Asn Gly Leu Glu Pro Leu Asp Pro
20 25 30

His His Val Lys Val Val Leu
35

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

Pro Thr Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Thr Ala Thr Leu
1

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

Val Thr Thr Gly Thr Asn Ile Ser Val Thr Thr Ala Met Arg Gln Glu
1 5 10 15

Gly Asn Arg Asn Phe Leu Pro Glu Ile Thr
20 25

(2) INFORMATION FOR SEO ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Leu Arg Trp Lys Tyr Ala Thr Cys Arg Glu Asn Ser Arg His Ala Thr
1 5 10 15

Ala Ile Val Val Leu Ser Glu Arg Ala Ala Lys
20 25

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

Trp Arg Thr Ala Asp Val Val Asp Ser Ala Ser Val Ala Ser Leu Thr
1 5 10 15

Pro Pro Pro Arg Ser Gly Arg
20

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Thr Pro Ser Arg Ser Leu Pro Val Pro Tyr Asp Pro Pro Pro Asn Pro
1 5 10 15
120

Leu Thr Pro Gly Tyr Asn Arg Trp Val Asn Leu Thr Pro Ser Arg Arg
 20 25 30

(2) INFORMATION FOR SEQ ID NO:344:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

Lys Arg Trp Asn Ala Tyr Leu Tyr Asn Arg Ala Glu Tyr Arg Cys Arg
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:345:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

Ser Arg Lys Ser Gly Lys Pro Gln Arg Ala Ala Leu Ile Ala Ala Ser
 1 5 10 15

Ala Thr Thr Ser Gly Leu Ser Leu
 20

(2) INFORMATION FOR SEQ ID NO:346:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Ser Lys Ala Ile Cys Leu Arg Arg Val Thr Val Lys Ile Ala Val Thr
 1 5 10 15

Thr Ala Ile Gln Met Pro Thr Pro Lys Pro Val Arg Ala Ala Phe Ala
 20 25 30

His Pro Ala Leu Ser Pro Gly Pro Asp Arg
 35 40

(2) INFORMATION FOR SEQ ID NO:347:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Pro Thr Arg Ile Val Thr Ala Ala Ala Ser Asp Ile Gly Ser Thr Asn
1 5 10 15

Ile Ser Glu Leu Lys Leu Ser Ala Ile
20 25

(2) INFORMATION FOR SEQ ID NO:348:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

Pro Ala Thr Ser Thr Ile Pro Asn Gly Glu Thr Ser Ser Ala Thr Thr
1 5 10 15

Ala Asn Asn Val Thr Ser Lys Asn Ser Gln Arg Asn Arg Gln Pro Gln
20 25 30

Leu Asn Gln Ala Leu His Asp Asp Ala Ile Gly Phe Ala Lys Ala Phe
35 40 45

Phe Ile Thr Asn Ile Thr His
50 55

(2) INFORMATION FOR SEQ ID NO:349:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

Thr Arg Val Phe Asn Val Arg Lys His Gly Asp Lys His His Pro Ile
1 5 10 15

Asp Arg Arg Ser Arg Asn Ala Ala Ala Asp Thr Ala Glu Phe Arg His
20 25 30

Thr Lys Met Ala Ile Asp Lys Asn Ile Val His Arg Asn Ile His Gln
35 40 45

Gln Ala Gln Lys Ser His His His Thr Arg Phe Gly Phe Gly Gln Thr
50 55 60

Phe Ala Leu Val Ser Arg Tyr Leu Lys Glu Lys Val Ser Cys Ala Pro
65 70 75 80

Gln Gln Arg Ala Lys Ile Thr His Gly Phe Ile Gly Gln Arg Arg Ile
85 90 95

Asn Ile Met His Arg Ala Asp Asn Val Ser Gly Ile Pro Gln Asp Asp
100 105 110

His His Gln His Gly Asp Lys Ala Arg Gln Pro Glu Pro Leu Ser Asn
115 120 125

Leu Met Arg Asp Thr Leu Thr Thr Ala Gly Ala Ile Glu Leu Arg Asn
130 135 140

His Arg Arg Gln Gly Gln Gln
145 150

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

Ala Val Thr Lys Gln Asn Gly Gly Lys Gln Ile Glu Val Pro Ile Ala
1 5 10 15

Thr Ala Ala Met Ser Val Ala Leu
20

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Pro Pro Ala Met Thr Val Ser Thr Asn Pro Leu Arg Ser Ile Pro Leu
1 5 10 15

Ala Gln Gly Ser Pro Val Ser Glu Arg
20 25

(2) INFORMATION FOR SEQ ID NO:352:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

Val Val Ile

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Lys Thr Lys Lys Pro Pro Lys Trp Gln Pro Lys Glu Ile Ala Gly Glu
1 5 10 15

Ile Ser Val Tyr Cys Ser Gly Val Leu Leu Phe Leu Gln
20 25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Lys Asn Ser Cys
1

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

Arg Arg Ile Ala Gly Lys Leu Phe Phe His Leu Leu Leu Cys
 1 5 10

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

Thr Val Leu Leu Leu Phe Ile Ser Gly Val Glu Asp Met Phe Thr Gly
 1 5 10 15

Ile Val Gln Gly Thr Ala Lys Leu Val Ser Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Ala Glu Pro Ser Gln Glu Gln Ile Asn Phe Phe Glu Gln Leu Leu Lys
 1 5 10 15

Asp Glu Ala Ser Thr Ser Asn Ala Ser Ala Leu Leu Pro Gln Val Met
 20 25 30

Leu Thr Arg Gln Met Asp Tyr Met Gln Leu Thr Val Gly Val Asp Tyr
 35 40 45

Leu Ala Arg Ile Ser Arg Arg Ser Met Pro Ser Ala
 50 55 60

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

His Gly Met Lys Val His Arg Ile Val Phe Leu Thr Val Leu Thr Phe
 1 5 10 15
 125

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Phe Leu Thr Ala Cys Asp Val Asp Leu Tyr Arg Ser Leu Pro Glu Asp
 20 25 30

Glu Ala Asn Gln Met Leu Ala Leu Leu Met Gln His His Ile Asp Ala
 35 40 45

Lys Lys Asn Arg Lys Arg Met Val
 50 55

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

Pro Tyr Val Ser Ser Ser Arg Gln Phe Ile Asn Ala Val Glu Ala Thr
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

Arg Leu Ser Ala
 1

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

Gly Ser Leu Gln Arg Arg Ile Arg Cys Phe Arg Leu Ile Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

Trp Tyr His Pro Arg Lys Asn Arg Gln Lys Ile Asn Phe Leu Lys Glu
1 5 10 15
Gln Arg Ile Glu Gly Met Leu Ser Gln Met Glu Gly Arg Asp
20 25 30

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

Pro Leu Arg Tyr Arg Leu Met Met Arg Glu Val Thr Leu Leu Arg Ala
1 5 10 15
Gln Leu Pro Tyr Leu
20

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

Asn Ile His Leu Arg Ser Ile Trp Arg Pro Phe Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

Lys Leu Lys Ile
1

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Arg Cys Gln Ser Leu Gly Cys Asn Thr Val Arg Leu Val Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:367:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Cys Ser Leu Leu Asn Ser Glu Trp
1 5

(2) INFORMATION FOR SEQ ID NO:368:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

Leu Thr Tyr Pro Arg Asp Lys His Ser Gly Leu Trp Thr Leu Ser Thr
1 5 10 15

Pro Ile Lys Gly Arg Trp
20

(2) INFORMATION FOR SEQ ID NO:369:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

Asn Thr Leu Ile Arg

1

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(2) INFORMATION FOR SEQ ID NO:370:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

Gln Asp Cys Tyr

1

(2) INFORMATION FOR SEQ ID NO:371:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

Glu Trp Ala Ser

1

(2) INFORMATION FOR SEQ ID NO:372:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

Ser Ala Ile Phe Ala

1

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(2) INFORMATION FOR SEQ ID NO:373:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Asp Ala Val Phe Glu Pro Thr

1

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(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

Ser Arg Gly Val Ala Thr Leu Ser Leu Phe Leu Ala Thr Cys Ser Leu
1 5 10 15
Arg Cys Thr Gly Met Ala Gly
20

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Ala Gly Leu Ser Ser Ser Asn Cys Trp Arg Tyr Gly Asp Arg Pro Glu
1 5 10 15
Leu Asp Arg Leu Leu Asp Arg Ala Leu Asn Arg Leu Arg Gly Ser Ser
20 25 30
Val Ile Pro Ala Cys Leu Asn Asp Arg Gln Lys Arg Gln Val Arg Leu
35 40 45
Ala Pro Arg Ile Ser Ala Phe Ala Phe Gly Leu Gly Leu Phe Lys Leu
50 55 60
Arg Cys Ser Asp Tyr Phe Met Leu Pro Glu Tyr Arg Gln Leu Leu Leu
65 70 75 80
Gln Trp Phe Ser Glu Asp Glu Ile Trp Gln Leu Tyr Gly Trp Leu Gly
85 90 95
Gln Arg Asp Gly Lys Leu Leu Pro Pro Gln Val Met Gln Gln Thr Ala
100 105 110
Leu Gln Ile Gly Thr Ala Ile Leu Asn Arg Glu Ala His Asp Asp Ala
115 120 125
Gly Phe Thr Cys Ala Ile Ser Ile Ile Thr Pro Ser Ala Ala Tyr Thr
130 135 140
Leu Ala Glu Asp Phe Ser Tyr Arg Asp Tyr Leu His Gly Ala Phe Ala
130

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145 150 155 160

Met Ser Phe Thr Ser Leu Pro Leu Thr Glu Ile Asn His Lys Leu Pro
 165 170 175

Ala Arg Asn Ile Ile Glu Ser Gln Trp Ile Thr Leu Gln Leu Thr Leu
 180 185 190

Phe Ala Gln Glu Gln Gln Ala Lys Arg Val Ser His Ala Ile Val Ser
 195 200 205

Ser Ala Tyr Arg Lys Ala Glu Lys Ile Ile Arg Asp Ala Tyr Arg Tyr
 210 215 220

Gln Arg Glu Gln Lys Val Glu Gln Gln Gln Glu Leu Ala Cys Leu Arg
225 230 235 240

Lys Asn Thr Leu Glu Lys Met Glu Val Glu Trp Leu Glu Gln His Val
 245 250 255

Lys His Leu Gln Asp Asp Glu Asn Gln Phe Arg Ser Leu Val Asp His
 260 265 270

Ala Ala His His Ile Lys Asn Ser Ile Glu Gln Val Leu Leu Ala Trp
 275 280 285

Phe Asp Gln Gln Ser Val Asp Ser Val Met Cys His Arg Leu Ala Arg
 290 295 300

Gln Ala Thr Ala Met Ala Glu Glu Gly Ala Leu Tyr Leu Arg Ile His
305 310 315 320

Pro Glu Lys Glu Ala Leu Met Arg Glu Thr Phe Gly Lys Arg Phe Thr
 325 330 335

Leu Ile Ile Glu Pro Gly Phe Ser Pro Asp Gln Ala Glu Leu Ser Ser
 340 345 350

Thr Arg Tyr Ala Val Glu Phe Ser Leu Ser Arg His Phe Asn Ala Leu
 355 360 365

Leu Lys Trp Leu Arg Asn Gly Glu Asp Lys Arg Gly Ser Asp Glu Tyr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

Asp Lys Asn Asp Ala Pro Tyr Ser Ile Tyr Pro Trp Pro Gly Tyr Arg
1 5 10 15

Gly Thr Arg Gly Tyr Phe Ala Phe Asn Val Ser Ser Pro Gly Val Thr
 20 25 30

Gly Asn Asp Gly Gly Ser Ala Leu
 35 40

(2) INFORMATION FOR SEQ ID NO:377:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

Asp Asp Gly Arg Asn Arg Asn Gly Ala Glu Trp
 1 5 10

(2) INFORMATION FOR SEQ ID NO:378:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

Thr Ala Arg Lys Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:379:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

Glu Thr Gly Ala Gln Thr Ala Gly Phe Ala Ala Phe Asp Lys Thr Asn
 1 5 10 15

Thr Gly Gly

(2) INFORMATION FOR SEQ ID NO:380:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

Trp Gly Asn Val Ala Ser Ala Tyr Arg Arg Glu
1 5 10

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

Phe Thr Glu Cys Val Ser Asn Tyr Arg Ser Cys Asn Gly Ala Tyr Cys
1 5 10 15

Arg Arg Val Val Lys Lys Glu Lys Thr Arg Phe Ala Ile Ala Thr Gly
20 25 30

Tyr Val Thr Ala Glu Glu Gly Trp Glu Leu Ala Val Phe Ser Leu Leu
35 40 45

Glu Leu Gly Glu Val Asp Thr Val Arg Cys Pro Leu
50 55 60

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

Ser Val Leu Cys Asn Arg Arg
1 5

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

Thr Thr Met Lys Cys Pro Tyr Arg Ser Gly Ser Asp Ala Trp Gln Thr
133

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1 5 10 15

Gly Arg Ile Ala Val Asn Gly Ser Val Phe Cys
20 25

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

Pro Leu Asn Leu Ala Tyr Ala Ser Asn Pro Arg Ser Lys Val Val Trp
1 5 10 15

Pro Gln His

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

Tyr Val Cys Val Val Cys Cys Tyr Ser Leu Ala Leu Lys Lys Ser Ala
1 5 10 15

Ser Val Arg Ser Gly Phe Ala Ser Cys Arg Leu Ile His Tyr Cys Arg
20 25 30

Tyr Tyr Ser Ile Leu Phe Val Ser Ala Gly Phe Ser Val Ile Gly Cys
35 40 45

Leu Ile Asp Leu Pro Leu
50

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

Phe Leu His Arg Arg Cys Ser Ile Gly Tyr Ser Asn Asn Leu Met Arg
1 5 10 15

Ser Leu Cys

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

Tyr Pro Ile Thr Val Leu Thr Thr Lys Ile Asn Val Asn Lys Phe Ser
1 5 10 15
Lys Arg Phe Val Lys
20

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

Ile Arg Phe Tyr Ser Asp Thr Trp Leu Ser Ile Phe Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

Ile Gly Phe Leu Ala His His Glu Ala Ser Gly Trp Ile Gly Ile Ser
1 5 10 15
Leu Leu Asn Val Ile Phe Ser Phe Leu Phe Asn
20 25

(2) INFORMATION FOR SEQ ID NO:390:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Leu Asn Gly Leu

1

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Gln Pro Ile Cys Ser Gly Gly Lys Asp Asn Met Lys Leu Ser

1

5

10

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

Arg Ser Tyr Ser Leu Met Ser Asp Thr Gln Ala Asn Leu Leu Arg Arg

1

5

10

15

Arg Thr Ala Phe

20

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

Leu Glu Thr Arg Ser Val Pro Gly Tyr Ser Ser Thr Ile Ile Phe Val

1

5

10

15

Ala Arg Trp Ala Cys Asn Glu Leu Phe Ser Thr Ser Phe Gln Leu Arg

20

25

30

Arg Ala Leu Val Thr Ile Thr Ser Ser Thr Asn Lys Ile Xaa Trp Ser

136

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35

40

45

Arg Asn Ala Phe Met Val Arg
50 55

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

Gly Ser Gln Gly Ala Thr Val Ala Gln Cys Met Arg Gly Ser Ala Gly
1 5 10 15

Tyr Gly Ser Gly Asp Gly Val Ile Asn Arg Tyr Cys Asp Asp Ala Val
20 25 30

Thr Leu Ala Asp Leu Asp Gly
35

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

Tyr Pro Asp Tyr Tyr Gln Pro Tyr Val Phe Ser Asp Pro Ala Leu Asn
1 5 10 15

Cys Tyr Leu Ser
20

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

Pro Ser Arg Phe Ile Gly Ile Ser Val Phe Ile Thr Tyr Tyr Tyr Ile
1 5 10 15

Ile Ser Phe Val Thr His Asn Gln His Ile Thr Ala Gly Thr Val Thr
137

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Thr

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

Tyr Cys Gly Cys Phe Arg

1

5

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Val Cys Arg Arg Arg Lys Ser His Arg Trp Val Gly Arg Ile Tyr His

1

5

10

15

His Tyr Tyr Arg Ala Ile Tyr Cys His Tyr Lys Arg Tyr Arg Glu Gly

20

25

30

Gly Gly Ser

35

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Arg Thr Phe Leu Ala

1

5

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

Trp Asp Ala Arg Gln Thr Asn Glu Tyr Arg Trp Arg Phe Ala Cys Arg
1 5 10 15
Ser Tyr Arg Cys Arg Pro Cys Pro Tyr Ile Lys Thr Ala Cys Pro Ala
20 25 30
Gly Lys Pro Leu Ser Arg Cys Asp Gly Arg Cys Asp Glu Ile Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

Arg Arg Tyr Asp Cys Arg Tyr Tyr Cys Cys Ser Gly Glu His Tyr Arg
1 5 10 15
Arg Tyr His Tyr Arg Tyr Arg Thr Ile
20 25

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Tyr Val Asp Glu
1

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

Gly Cys Ser His Leu
1 5

(2) INFORMATION FOR SEQ ID NO:404:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

Asp Phe Pro

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

(2) INFORMATION FOR SEQ ID NO:406:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Thr Ser Val Ala His Ile Asn Arg Cys Gly Phe Asn Ala Pro Arg Phe
20 25 30

Asn Ser Trp Leu Ser Phe Tyr His Ser Arg Phe Leu Phe Ser Val Val
35 40 45

Ser Ile Ala Asn Tyr Pro His Ser Pro Gln Lys Val Cys Gly Phe Arg
50 55 60

Lys Trp Arg Arg Ser Thr Gly Lys Arg

65

70

(2) INFORMATION FOR SEQ ID NO:407:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Tyr Gly Ser Arg Arg Met Ser Ser Asn Leu Thr Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:408:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

Pro Asp Val Thr Phe Cys Arg Pro Asp Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:409:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Arg His Glu Met Val Phe Ile
 1 5

(2) INFORMATION FOR SEQ ID NO:410:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

Gly Tyr Arg Arg Pro Ser Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

Thr His Arg Lys Ile Asp Gly Thr Ala Ile Ser Gly Thr Arg Ile
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

Phe Ile Tyr Ser Arg Ser Gly Gly Leu Phe Ile Asp Arg Arg Gly Arg
1 5 10 15

(2) INFORMATION FOR SEO ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

Gln Pro Asp Val Thr Glu Arg Asp Gly Ala Asp Leu Leu Ala Tyr Lys
1 5 10 15

Arg His Gly Pro
20

(2) INFORMATION FOR SEO ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Gly Ala Arg Phe Trp Thr Gly Arg Phe Arg Gly Gln Pro Thr Tyr Leu
1 5 10 15

Cys Leu Ile Lys Met Cys Pro Ala Ser Ala Tyr Gly Arg Val Tyr Trp
20 25 30

Cys Ser Gly Asn Ala Leu Ser Asn Glu Cys Asp Gly Lys Lys Leu Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

Ala Gly Glu Arg Ala Ser Ala Pro Val Thr His
1 5 10

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

Asn Phe Ala Thr Ala Cys Ile Arg Ala Gly Phe Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

Arg Phe Thr Ser Tyr Phe Arg His Leu Asn
1 5 10

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

Leu Gly Ala Thr

1

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

Lys Arg Cys Pro Asp Val Asp Arg Ile Cys Pro Tyr Arg Ala Ser Ser

1

5

10

15

Ser Tyr Ser Ala Ser Ser

20

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Ser Gly Arg Lys Thr Ala Ala Asp Phe Ala Asp Arg Arg Arg Tyr

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

Lys Pro Arg Ala

1

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

Ile His Ser Pro Asp Gly Asn Gly Asp Leu Tyr Cys Ala Val Val Ser
 1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

Asp Ala Asp Pro Ala Thr Tyr Arg Ala Gly Ala Glu Ala Val Ser Gln
 1 5 10 15

Ile Ile His Cys His Phe Cys Arg His Pro Thr Phe Leu Ala Lys Asn
 20 25 30

Tyr Arg Ser His Leu Val Arg Arg Thr Asp Phe Val Met Ala Gly Ile
 35 40 45

Arg Arg Gly Glu Pro Tyr Thr Ser Gly Arg Lys Tyr
 50 55 60

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Arg Arg Gly Val Gly Gly Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Asn Ile Arg Pro Pro Met Val Ile Val Asp Gly Ala Glu Phe Arg Met
1 5 10 15
Ser Ala Gln Arg Cys
20

(2) INFORMATION FOR SEQ ID NO:426:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

Met Arg Gly Cys Leu Gly Tyr Leu Trp Ala Ser Cys Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:427:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

Ser Leu Glu Lys Asn Leu Leu Lys Ser Trp Gly Leu Met Ala Ala Lys
1 5 10 15

Leu Cys Tyr Leu Leu Arg Val Gln Ser Gly Phe Thr Ala Gly Ser
20 25 30

Lys

(2) INFORMATION FOR SEQ ID NO:428:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Ala Thr Pro Ser Gly Ser Arg Gly Arg Ser Val Ile Arg Ala Ser Tyr
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:429:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Trp Leu Trp Ser Ser Pro
 1 5

- (2) INFORMATION FOR SEQ ID NO:430:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

Trp Pro Arg Thr Ala Arg Arg Leu Leu Glu Arg Leu
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:431:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

Cys Asn Ala Ser Ser Arg Asn Gly Ser Thr Ala Tyr His Ser Thr Ile
 1 5 10 15

Asn Asp Gly Asp Ser Arg Tyr
 20

- (2) INFORMATION FOR SEQ ID NO:432:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

Arg Cys Asp Leu Trp Arg Arg Ala Thr Ser Gly Tyr Phe Phe Cys Ser
 1 5 10 15

Trp Arg Gly Glu Lys His Ala Ser Gly Asp Ala Val
20 25

(2) INFORMATION FOR SEQ ID NO:433:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

Cys Ala Arg Arg Arg Gln Gln Cys Ser Gly Val Asn Trp
1 5 10

(2) INFORMATION FOR SEQ ID NO:434:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

Thr Trp Thr Arg Ser Pro Arg Ile His Arg Phe Tyr Thr Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:435:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

Arg Asp Pro Lys Thr Leu Cys His Cys Cys Arg Asn Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:436:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

Gln Thr Arg Leu Arg Ala Arg Glu Gly Ala Val Cys Gly His His Asp
 1 5 10 15

Ser Arg Ile Phe Ser Arg
 20

(2) INFORMATION FOR SEQ ID NO:437:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

Trp Lys Ala Ser Arg Leu Ala Cys Arg Leu Thr Asp Ala Leu Cys Gln
 1 5 10 15

Gly Arg Thr Glu Ile Ala Leu Ala Pro Glu Arg Pro Arg Phe Leu Glu
 20 25 30

Asn Ile Ala Arg Arg Ile
 35

(2) INFORMATION FOR SEQ ID NO:438:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

Cys Ile Ala Thr Thr Phe Arg Thr Tyr Gly Asn Gly Arg Lys Arg Gln
 1 5 10 15

Tyr Tyr Arg Ile Leu Tyr Gly Thr Gly Gly Arg Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

Ser Arg Trp Arg Met Lys Ser Val His Cys Leu Met Asp Ile Leu Tyr
 1 5 10 15

Tyr Pro Asp Gly Leu Gln Arg Gly Gly Ile Ile Leu Pro Leu Thr Cys
 20 25 30
 Trp Gln Arg Ser Ala Ala Phe Phe Gln Ser Leu Pro Ala Met Ser Ile
 35 40 45
 Val Asn Trp Arg Arg Tyr Cys Asp Gly Ala Trp Arg Phe Thr Arg Arg
 50 55 60
 Leu Asn Cys
 65

(2) INFORMATION FOR SEQ ID NO:440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

Tyr Ala Leu Gly Asn Thr Ser Glu Glu Leu Ile Gln Ile Leu Thr Lys
 1 5 10 15
 Pro Leu Ile Pro Ile Arg Ile Phe Ala His Phe Cys Asp Lys Val Arg
 20 25 30
 Met Lys Tyr Ala Asp Pro Ser Tyr Leu
 35 40

(2) INFORMATION FOR SEQ ID NO:441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

Lys Asn Tyr Thr Lys Tyr Ser Pro Ser Asp His Gly Asn Phe Ala Gly
 1 5 10 15
 Asp Asn Arg Ala Ala Glu Lys Gln Leu Arg Gly Lys Leu Thr Val Leu
 20 25 30
 Asp Gln Gln Gln Gln Ala Ile Ile Thr Glu Gln Gln Ile Cys Gln Thr
 35 40 45
 Arg Ala Leu Ala Val Ser Thr Arg Leu Lys Glu Leu Met Gly Trp Gln
 50 55 60
 Gly Thr Leu Ser Cys His Leu Leu Leu Asp Lys Lys Gln Gln Met Ala
 65 70 75 80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

Ser Val Lys Tyr Val Asn Gln Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:445:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

Glu Ser Met Ser Leu Ile Met Lys Phe Thr Val Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

Ser Ser Gly Trp Ser Leu Ser Cys Cys Ile Trp Gly Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

Phe Pro Trp Arg Tyr Ser Met Leu Arg Ile Ala Asn Glu Glu Arg Pro
1 5 10 15

Trp Val Glu Ile Leu Pro Thr Gln Gly Ala Thr Ile Gly Glu Leu Thr
20 25 30

Leu Ser Met Gln Gln Tyr Pro Val Gln Gln Gly Thr Leu Phe Thr Ile
35 40 45

Asn Tyr His Asn Glu Leu Gly Arg Val Trp Ile Ala Glu Gln Cys Trp
50 55 60

Gln Arg Trp Cys Glu Gly Leu Ile Gly Thr Ala Asn Arg Ser Ala Ile
152

65		70		75		80									
Asp	Pro	Glu	Leu	Leu	Tyr	Gly	Ile	Ala	Glu	Trp	Gly	Leu	Ala	Pro	Leu
			85						90					95	
Leu	Gln	Ala	Ser	Asp	Ala	Thr	Leu	Cys	Gln	Asn	Glu	Pro	Pro	Thr	Ser
			100					105					110		
Cys	Ser	Asn	Leu	Pro	His	Gln	Leu	Ala	Leu	His	Ile	Lys	Trp	Thr	Val
		115					120					125			
Glu	Glu	His	Glu	Phe	His	Ser	Ile	Ile	Phe	Thr	Trp	Pro	Thr	Gly	Phe
	130					135					140				
Leu	Arg	Asn	Ile	Val	Gly	Glu	Leu	Ser	Ala	Glu	Arg	Gln	Gln	Ile	Tyr
145				150						155					160
Pro	Ala	Pro	Pro	Val	Val	Val	Pro	Val	Tyr	Ser	Gly	Trp	Cys	Gln	Leu
				165					170					175	
Thr	Leu	Ile	Glu	Leu	Glu	Ser	Ile	Glu	Ile	Gly	Met	Gly	Val	Arg	Ile
			180					185					190		
His	Cys	Phe	Gly	Asp	Ile	Arg	Leu	Gly	Phe	Phe	Ala	Ile	Gln	Leu	Pro
		195					200					205			
Gly	Gly	Ile	Tyr	Ala	Arg	Val	Leu	Leu	Thr	Glu	Asp	Asn	Thr	Met	Lys
	210					215					220				
Phe	Asp	Glu	Leu	Val	Gln	Asp	Ile	Glu	Thr	Leu	Leu	Ala	Ser	Gly	Ser
225				230						235					240
Pro	Met	Ser	Lys	Ser	Asp	Gly	Thr	Ser	Ser	Val	Glu	Leu	Glu	Gln	Ile
			245						250					255	
Pro	Gln	Gln	Val	Leu	Phe	Glu	Val	Gly	Arg	Ala	Ser	Leu	Glu	Ile	Gly
			260					265					270		
Gln	Leu	Arg	Gln	Leu	Lys	Thr	Gly	Asp	Val	Leu	Pro	Val	Gly	Gly	Cys
	275						280					285			
Phe	Ala	Pro	Glu	Val	Thr	Ile	Arg	Val	Asn	Asp	Arg	Ile	Ile	Gly	Gln
	290					295					300				
Gly	Glu	Leu	Ile	Ala	Cys	Gly	Asn	Glu	Phe	Met	Val	Arg	Ile	Thr	Arg
305				310						315					320
Trp	Tyr	Leu	Cys	Lys	Asn	Thr	Ala								
			325												

- (2) INFORMATION FOR SEQ ID NO:448:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Tyr Ala Asn Asn Ile Ile Ala Phe Gln Val Val Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Glu Ile Gln Tyr Val Phe Thr Arg Phe Ala Phe Ala Thr Asp Trp Tyr
1 5 10 15

Ile Val Ser Ala Phe Asn Thr Ala Ser His Tyr Arg His Gly Asn Phe
20 25 30

Phe Pro

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Thr Gly Gly Gly Ile Phe Asp Phe Thr Lys Cys Ser Gly Tyr Ser Thr
1 5 10 15

Ser Pro Pro Lys Tyr Arg Thr Val Trp Pro Cys Ala Cys Thr Phe Leu
20 25 30

Ile His Tyr Gly Ala Asp Ala Ile Ser Cys Lys Arg Ala Leu Ala Ser
35 40 45

Gly Ser Gly Arg Trp Arg Ser Phe Leu Asp Val
50 55

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

Ser Ile Ser Ala Leu Ser Thr Val Phe Ala Lys Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:452:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Arg Glu Gly Ser Gln Leu Phe Ser Glu Phe Asp Lys Thr Asn Leu Ala
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:453:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

Arg His Lys Lys Lys Asp Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:454:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

Phe Phe Ala His Ile Asn Ser Gly Ile Tyr Gly Glu Ser Val Asn Ala
1 5 10 15

Gly Ile Ser Asp Trp Ile Thr Tyr Leu Ser Ser Leu Ser Gly Tyr
20 25 30

(2) INFORMATION FOR SEQ ID NO:455:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

Pro Ala Tyr Phe Lys Tyr Thr Ala Gly Tyr Gly Asp Asp Asp Gly Val
1 5 10 15
Ala Asp Asp His Phe Ile Thr Val
20

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

Ala Ala Asn Ile Phe Thr Gly Arg Arg Leu Gly Ser Asp Thr Gly Ala
1 5 10 15
Ile Gly Thr Glu Leu Phe Met Asn Asp Ser Glu Leu Thr Gln Phe Val
20 25 30
Thr Gln Leu Leu Trp Ile Val Leu Phe Thr Ser Met Pro Val Val Leu
35 40 45
Val Ala Ser Val Val Gly Val Ile Val Ser Leu Val Gln Ala Leu Thr
50 55 60
Gln Ile Gln Asp Gln Thr Leu Gln Phe Met Ile Lys Leu Leu Ala Ile
65 70 75 80
Ala Ile Thr Leu Met Val Ser Tyr Pro Trp Leu Ser Gly Ile Leu Leu
85 90 95
Asn Tyr Thr Arg Gln Ile Met Leu Arg Ile Gly Glu His Gly
100 105 110

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

Met Ala Gln Gln Val Asn Glu Trp Leu Ile Ala Leu Ala Val Ala Phe
1 5 10 15

Ile Arg Pro Leu Ser Leu Ser Leu Leu Leu Pro Leu Leu Lys Ser Gly
20 25 30

Ser Leu Gly Ala Ala Leu Leu Arg Asn Gly Val Leu Met Ser Leu Thr
35 40 45

Phe Pro Ile Leu Pro Ile Ile Tyr Gln Gln Lys Ile Met Met His Ile
50 55 60

Gly Lys Asp Tyr Ser Trp Leu Gly Leu Val Thr Gly Glu Val Ile Ile
65 70 75 80

Gly Phe Ser Ile Gly Phe Cys Ala Ala Val Pro Phe Trp Ala Val Asp
85 90 95

Met Ala Gly Phe Leu Leu Asp Thr Leu Arg Gly Ala Thr Met Gly Thr
100 105 110

Ile Phe Asn Ser Thr Ile Glu Ala Glu Thr Ser Leu Phe Gly Leu Leu
115 120 125

Phe Ser Gln Phe Leu Cys Val Ile Phe Phe Ile Ser Gly Gly Met Glu
130 135 140

Phe Ile Leu Asn Ile Leu Tyr Glu Ser Tyr Gln Tyr Leu Pro Pro Gly
145 150 155 160

Arg Thr Leu Leu Phe Asp Gln Gln Phe Leu Lys Tyr Ile Gln Ala Glu
165 170 175

Trp Arg Thr Leu Tyr Gln Leu Cys Ile Ser Phe Ser Leu Pro Ala Ile
180 185 190

Ile Cys Met Val Leu Ala Asp Leu Ala Leu Gly Leu Leu Asn Arg Ser
195 200 205

Ala Gln Gln Leu Asn Val Phe Phe Phe Ser Met Pro Leu Lys Ser Ile
210 215 220

Leu Val Leu Leu Thr Xaa
225 230

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Ser His Ser Leu Met Leu Phe Ile Thr Ile Trp Leu Lys Ala Ile Asn
1 5 10 15

Phe Ile Phe Ile

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

Lys Thr Gly Phe His Leu Tyr Glu Arg Glu Asn Arg Thr Ala Tyr Arg
 1 5 10 15

Lys Glu Ile Thr
 20

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Gly Arg Ala Gly Cys Gln Lys Tyr
 1 5

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

Asn Asn Ile Ile Ile Ser Ala Asp Cys Ala Leu Phe Val Phe Ser Phe
 1 5 10 15

Leu Tyr

(2) INFORMATION FOR SEQ ID NO:462:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

Lys Asp Asp Phe Asp Thr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:463:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

Val Asn Asn Phe His Ile Thr Ile Ser Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:464:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Thr Ile Phe Leu Cys Ile Asn Ala Ile Glu Ser Cys Phe Asn Arg Val
1 5 10 15

Thr Asp Phe Cys Thr Ala Val Ser Gly Arg Trp Gly Asn Ser Cys Tyr
20 25 30

Cys Gly

(2) INFORMATION FOR SEQ ID NO:465:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Arg Val Ser Ser Gly Gly Gly Tyr Cys Gln Gln Gly His Trp Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

Lys Arg Ala Tyr Lys Ser Gly Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

Ala Asp Ile Leu Phe Thr
 1 5

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Arg Ser Arg Ile Met
 1 5

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Ile Gln Pro Lys Ser Tyr His Ala Ile Ser Tyr Leu Cys Leu Phe Leu
 1 5 10 15

Leu Leu Leu Cys Gln Tyr Phe Ser Gly Ala Thr Val Leu Trp Val Ser
 20 25 30

Leu Trp Arg Ala Cys Gly Phe Phe Phe Asn Lys Met Val Met Gly Arg
 35 40 45

Gly Asp Gly Phe Leu Tyr Arg Arg Trp His Thr Gly Leu Phe Phe Ser
 50 55 60

Ile Leu
 65

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

Lys Ser Tyr Leu Lys Met Ser Lys Asp Asp Val Lys Gln Glu His Lys
 1 5 10 15

Asp Leu Glu Gly Asp Pro Gln Met Lys Thr Arg Arg Arg Lys Cys Arg
 20 25 30

Val Lys Tyr Lys Val Gly Val
 35

(2) INFORMATION FOR SEQ ID NO:471:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

Leu Asn Leu Leu Asn Asn Leu Leu Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:472:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

Cys Val Ile Gln Arg Ile Leu Arg Phe Val Leu Ala Ile Ile Pro Pro
 1 5 10 15

Ile Cys Gln Tyr His Ala Ser Trp Lys Lys Ala Val Met Leu Lys Leu
 20 25 30

Thr Ile Leu Leu Thr Ser Leu Asn Ala Thr Ala Ser Pro Leu Leu Lys
 35 40 45

Met Leu Ser Trp Pro Ala His Tyr Phe Leu Lys Trp Asn Ala Glu Ile
 50 55 60

Lys Phe Leu Lys Arg Tyr Leu Asn Pro Leu Gln Pro Cys Tyr Val Trp
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

Ile Met Arg Ile Leu Pro Lys His His Lys Cys Phe Trp Tyr Ala Ser
 1 5 10 15

Ser Gly His Cys Glu Gly
 20

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

Glu Gly Asn Ser Val
 1 5

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Glu Thr Glu Asn Asn Arg Phe
 1 5

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

Pro Gly Thr Ser Thr Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:477:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

Arg Ile Ile Lys Leu Asn Lys Ile Met Asp Trp Cys Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:478:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Asp Ser Asn His Ser Thr Pro Thr Met Ser Arg Trp Cys Ser Asn
 1 5 10 15

Gln Leu Ser Tyr Glu Arg Gln Arg Cys Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:479:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

Gln Arg Gly Arg Ile Leu Ala Ser Gln Pro Gln
 1 5 10

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(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

Gly Lys Arg Glu Ile Ala Ile Phe Phe Leu Lys Ser Pro Asp Cys Gly
1 5 10 15
Gly Asn Met Gln His Val Glu Lys Ile Ala Ala Met Arg Arg Leu Ser
20 25 30
Ser Tyr Tyr Arg Ser Ala Leu Gln Asn Asp Gly Gly Arg Leu Thr Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

Ile Ala His Pro
1

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

His Arg Arg Arg Gly Gln Ala Asp Asp Glu Pro His Pro Glu Ala Cys
1 5 10 15
Arg Ser His Thr Ile His His Gln Ile Arg
20 25

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

Arg Gln Asp Ile Thr Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

His Pro Val Gly Gly Lys Gly Asp Lys Lys Asp Gly Thr Arg Ile Phe
1 5 10 15

Ile Thr Ala Gln Asn Thr Ala Ala Asp Asn Leu Tyr Arg Val Gly Asn
20 25 30

Leu Val Asn Arg Ser Glu Gln His
35 40

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

Leu Arg Gln Ala Pro Arg Pro Gln Gly Cys His Cys Arg Ala Lys Gln
1 5 10 15

Tyr Ala Tyr Ala Glu
20

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein
(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Pro Gln Pro Tyr Lys Cys Arg Arg Leu Asn Arg Tyr Ala Leu Arg Leu
165

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1 5 10 15

Arg Ile Gln Arg
20

(2) INFORMATION FOR SEQ ID NO:487:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

Ala Leu Ala Gln Thr Asp Asn Pro Leu Glu Ser Leu Pro Pro Gln Pro
1 5 10 15

Ala Thr Ser Ala Val Arg Thr Ser Ala Ser
20 25

(2) INFORMATION FOR SEQ ID NO:488:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Ala Gln Ser Asp Asp Arg Arg His Pro Gln Tyr Leu Met Ala Lys Pro
1 5 10 15

Ala Ala Gln Arg Pro Gln Ile Thr Ser Leu Gln Arg Thr Ala Ser Ala
20 25 30

Ile Gly Asn Pro Ser
35

(2) INFORMATION FOR SEQ ID NO:489:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

Ile Arg Arg Phe Met Thr Thr Leu Ser Gly Leu Pro Lys Pro Phe Ser
1 5 10 15

Leu Arg Ile Ser Arg Ile Glu Arg Ala Cys Leu Met
166

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(2) INFORMATION FOR SEQ ID NO:490:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Glu Ser Met Ala Ile Asn Ile Thr Gln
 1 5

(2) INFORMATION FOR SEQ ID NO:491:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

Thr Ala Ala Val Ala Thr Pro Gln Pro Ile Pro Pro Ser Ser Gly Ile
 1 5 10 15

Pro Lys Trp Pro
 20

(2) INFORMATION FOR SEQ ID NO:492:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

Phe Thr Gly Ile Phe Thr Ser Arg Pro Lys Asn Pro Ile Thr Ile Pro
 1 5 10 15

Gly Leu Val Leu Ala Arg Pro Ser His Trp Phe Arg Ala Thr
 20 25 30

(2) INFORMATION FOR SEQ ID NO:493:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

Lys Lys Arg Tyr Pro Ala Pro His Ser Ser Ala Arg Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Pro Thr Ala Leu Ser Ala Ser Ala Gly Ser Ile Leu Cys Ile Glu Arg
1 5 10 15

Ile Met Tyr Pro Ala Phe His Arg Thr Ile Ile Thr Ser Thr Glu Thr
20 25 30

Lys Pro Ala Ser Gln Asn Pro Cys Arg Thr
35 40

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Cys Ala Ile Arg Ser Arg Arg Pro Glu Pro Leu Ser Cys Ala Ile Thr
1 5 10 15

Gly Val Lys Ala Ser Ser Lys Pro
20

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Pro Asn Lys Met Ala Gly Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:497:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

Arg Arg Gln Pro Cys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:498:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Arg Tyr Ser Leu Pro Pro
1 5

(2) INFORMATION FOR SEQ ID NO:499:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Arg Tyr Arg Arg Ile His Cys Gly Leu Tyr His Leu Arg Lys Asp His
1 5 10 15

Arg Tyr Leu Asn Ala Asn Asn
20

(2) INFORMATION FOR SEQ ID NO:500:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

Arg Ala Ser Leu Val Tyr Phe Cys Thr Tyr Ser Pro Phe Ile Leu Leu
 1 5 10 15

Leu Tyr Glu Arg Leu Lys Ser Arg Arg Ser Gly Ser Gln Lys Lys
 20 25 30

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

Gln Gly Lys Phe Gln Ser Ile Val Ala Gly Tyr Tyr Tyr Phe Ser Ser
 1 5 10 15

Glu Lys Thr Val Val Asn Gly Ala Leu Leu Ala Ser Cys Phe Ser Thr
 20 25 30

Cys Tyr Cys Ala Glu Gln Phe Cys Phe Tyr Leu Phe Gln Glu Leu Lys
 35 40 45

Ile Cys Leu Arg Gly Ser Tyr Arg Val Pro Arg Asn Trp Tyr Arg
 50 55 60

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